U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

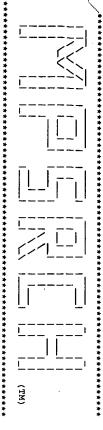
#### **SEARCH REQUEST FORM**

5-54

Requestor's Name:		Serial Number:		
Date:	Phone:	Aı	t Unit:	
Search Topic: Please write a detailed statement of sea terms that may have a special meaning please attach a copy of the sequence. Y	. Give examples or relevent cit	tations, authors, keywor	rds, etc., if known. For se	Define any equences,
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	STAFF USE	ONLY		
Date completed: 5-7-98  Searcher: MARK  Terminal time: 6  Elapsed time: 700  CPU time: 700  Total time: 700  Number of Searches: 700	Search Type of		Vendors  STN Dialog APS Geninf SDC	
Number of Databases:		Structure Bibliographic	DARC	/Questel

PTO-1590 (9-90)

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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed May 6 08:18:28 1998; MasPar time"3.90 Seconds 375.094 Million cell updates/sec

Description: Perfect Score: >US-08-804-166-2 (1-256) from US08804166.pep 1994

Sequence: 1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150 Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-1ssued 1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 29.680; Variance 124.309; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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REPLICANT: WALLACH, DAVI APPLICANT: WALLACH, DAVI APPLICANT: WARFOLOMEEV, APPLICANT: BAKKBUSCH, ( APPLICANT: BAKKBUSCH, ( APPLICANT: BAKKIN, Mich TITLE OF INVENTION: MOLL TITLE OF INVENTION: THE NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS: 42 CORRESPONDENCE ADDRESS: 42 CORRESPONDENCE ADDRESS: 42 CORREST: 419 Seventh St CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPy di COMPUTER: IBM PC compopERATING SYSTEM: PC-I COUNTRY: DATA: APPLICATION NUMBER: US FILING DATE: 12-OCT-I CASSIFICATION: 435 CLASSIFICATION UMBER: II FILING DATE: 12-OCT-I TILING DATE: 12-OCT-I ATTORNEY/AGENT INFORMATION NAME: BROWDY, ROGER L. REFERENCE/DOCKET NUMBER: TELEPHONE: 202-628-51; TELEPHONE: 202-737-3528 TELEPHONE: 202-737-3528	rada, ,			68-2	777888888888888999999
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Best Local 9
                                            ATTORNEY/AGENT INFORMATION:
NAME: ROBbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
 SEQUENCE
                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/ACERTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
MOLECULE TYPE: protein
JENCE 455 AA; 50579 MW; 1048388 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 455 AA; 50494 MW; 1048031 CN;
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
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                                TYPE: amino acid
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                        TOPOLOGY:
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CITY: Palo Alto
STATE: Californ:
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Similarity 99.3%;
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Pred. No. 1.28e-100;
1; Mismatches 0; Indels
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                                                                             SEQUENCE
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41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Local Similarity 99.3%;
                                                                                                                                             TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: '
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-Msy-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                              STREET: OJCITY: Palo Alto CITY: Palo Alto CTATE: California
                                                                                                                                                                  TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                      MOLECULE TYPE:
                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
                                                                                                LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                         NAME: ROBbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 51
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142;
                                            Similarity
                                                                            LE TYPE: protein
199 AA; 22186 MW; 195553 CN;
                                                                                                                                                                                                                                                                                                                                     94301
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                                            98.68;
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                                          Score 1115; DB 7;
Pred. No. 1.05e-99;
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Pred. No. 1.28e-100;
                                                                                                                                                                                           5150-0030
                                  Mismatches
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 143
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Patent No.
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                             161 KONTVCT 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: M.Feldmann, P.W. Gray, APPLICANT: M.J.C. Turner, F.M Brennan
                                                                                                                DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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                                                                          SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
 KONTVCT 149
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                                                          SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94301
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1 Similarity 100.0%;
127; Conservative
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o. 5633145
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167 AA; 18626 MW; 139513 CN;
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: California
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(415) 327-3231
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Pred. No. 1.15e-87;
0; Mismatches 0;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                / Match 49.9%;
Local Similarity 100.0%;
hes 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
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                                                                                                                                                                             SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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167 AA; 18626 MW; 139513 CN;
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                                                        STANDARD;
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Pred. No. 1.15e-87;
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  Sequence 50, Application US/08050319B
Patent NO. 5633145
GENERAL INFORMATION:
APPLICANT: M.Teldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08050319B Patent No. 5633145
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Local Similarity 100.0%;
hes 124; Conservative
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APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECHOME: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144
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APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
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MEDIUM TYPE: Floppy disk
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JENCE 124 AA; 14047 MW; 75840 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
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635 Bryant Street
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Pred. No. 3.78e-86;
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REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LEGGT: 157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54, Application US/08050319B.
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                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                       STREET: OJUNE CITY: Palo Alto CITY: California
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ATTORNEY/AGENT INFORMATION:
NAME: RODDING, RODETTA L
                                                                                                                                                                                                                                                APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 157 AA; 17570 MW; 122247 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
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                                                                      ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 635 Brya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993
                                                                                                                                                                                        ADDRESSEE:
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1 Similarity 96.2%;
102; Conservative
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635 Bryant Street
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Pred. No. 6.45e-68;
2; Mismatches 2;
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Best Local
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INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE 158 AA; 17375 MW; 124033 CN;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 52, Application US/08050319B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-050-319B-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-193
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBDINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                     Patent No. 5633145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     Sequence 52, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 SCSKCRKEMGQVEISSCTVDRDTVCTCH 128
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Local Similarity 97.7%;
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SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CIACTERIA STATE
                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                 APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RObbins, Roberta L
                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                     STREET: 635 Bryant
CITY: Palo Alto
STATE: California
                                                                                                                                                                                               ZIP: 94301
                                                                                                                                                                                                          COUNTRY:
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Pred. No. 1.67e-54;
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Best Local S
Matches 6
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 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENCTH: 153 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
EQUENCE 153 AA; 17148 MW; 116104 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 23.9%;
Local Similarity 66.0%;
hes 66; Conservative
                                                                                TELEFAX: (415) 327-32
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 CPQGKYIHPQNN-SIC--CTKCHK--GTYLYNDCPGPGQDT-DCRKNQYRHYWSENLFQC 97
        LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Meccosis Factor alpha) Recepton
NUMBER OF SEQUENCES: 57
                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 617-8999
                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/050,319B
FILING DATE: 10-May-1993
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
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LE TYPE: peptide
41 AA; 4856 MW; 8601 CN;
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Pred. No. 8.82e-36;
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Query Match 17.0%; Best Local Similarity 100.0%;

Score 339; DB 7; Pred. No. 2.30e-22;

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FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                        TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 40 AA; 4459 MW; 7536 CN;
Sequence 31, Application US/08050319B
                           01-JAN-1900
                                                 XXXXXX
                                                                      US-08-050-319B-31
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GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
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                                                                                                                / Match 16.2%;
Local Similarity 100.0%;
nes 40; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVC 41
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California
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                                                                     STANDARD;
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Pred. No. 6.30e-21;
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                                                                                                                                                                      Sequence 2, Application US/08292549
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                                                                                                                                    Sequence 2, Application US/08292549 Patent No. 5464938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/08050319B Patent No. 5633145 GENERAL INFORMATION:
                                                                         GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goddin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                      65 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 107
                                                                                                                                                                                                                                                                                                   1 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
                                                      ADDRESSEE: Immunex C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 617-8999
                      STATE:
                                            STREET:
           COUNTRY:
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43 AA; 4767 MW; 9758 CN;
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Palo Alto
California
                                 Seattle
                    Washington
                                          51 University Street
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                                                        Immunex Corporation
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE 325 AA; 35132 MW; 591446 CN;
                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9102207.
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                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9102207 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY 111
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LIAL-LYCVYYYYGDDYPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLAFGLICLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC
                                                                                                  ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/90
FILING DATE: 10/19/92
ATTORNEY/AGENT INFORMATION:
                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/022/
FILING DATE: 19910329
                                                                                                                                                                                              APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,633
REFERENCE/DOCKET NUMBER: 261
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1 CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION: NAME: Wight, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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39; Conser
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51 University Street
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SYSTEM: PC-DOS/MS-DOS
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34.8%;
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                                               PCT/US91/02207
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Pred. No. 1.31e-11;
21; Mismatches 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xxxxx
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08292549 Patent No. 5464938 GENERAL INFORMATION:
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les 39; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 587-060
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                        TELEFAX: (206) 233-06
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 RECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY 114
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                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/96:
FILING DATE: 10/19/92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LIAL-LYCVYYYYGDDYPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LLAFGLLCLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID
TOPOLOGY: 1100
                                                                                                                                                                                                                                                                                                                             APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                            REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 260
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        STREET: Seattle
NAME: Perkins, Patricia A REGISTRATION NUMBER: 34,69
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                            FILING DATE
                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       STATE: Washington
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325 AA; 35132 MW; 591446 CN;
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                    326 amino acids
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587-0606
-- NO: 2:
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Pred. No. 1.31e-11;
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 10:00:45 1998; MasPar time 59.61 Seconds 927.602 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence:
Comp: >US-08-804-166-1 (1-1049) from US08804166.seq 1049 1 TCCACATGGCTACAGGTAAG......TTATTATCACAAATCTTAAG 1049
AGGTGTACCGATGTCCATTC.....ATAATAGTGTGTTTAGAATTC

Scoring table: TABLE default Gap 6

Nmatch

STD:

Dbase 0; Query 0

Searched: 102136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: n-issued 1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96 Mean 8.672; Variance 4.371; scale 1.984

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	Length	Bd	Ħ	Description	Pred. No.
1	424	40.4	2062	7	us-08-050-	Sequence 24, Applicati	0.00e+00
ນ	424	40.4	2175	7	-80-	1, A	0
ω	424	40.4	6889	σ	US-08-286-	Sequence 2, Applicatio	0
4	424	40.4	6889	14	PCT-US95-0	2	0
ഗ	420	40.0	600	7	US-08-050-	Sequence 47, Applicati	0
0	381	36.3	504	7	us-08-050-	Sequence 56, Applicati	
7	379	36.1	501	7	us-08-050-	Sequence 1, Applicatio	0
œ	370	35.3	372	7	US-08-050-	Sequence 3, Applicatio	
ဖ	302	28.8	474	7	US-08-050-	Sequence 49, Applicati	ω
10	300	28.6	2771	7	US-08-273-	Sequence 5, Applicatio	ᆫ
11	298	28.4	4283	7	US-08-343-	Sequence 3, Applicatio	8.01e-221
12	298	28.4	4283	7	US-08-445-	Sequence 1, Applicatio	~ @
13	255	24.3	477	7	US-08-050-	Sequence 53, Applicati	7
14	169	16.1	462	7	US-08-050-	51,	1.18e-
15	69	6.6	534	σ	US-08-187-	Sequence 3, Applicatio	
16	69	6.6	654	σ	US-08-187-	Sequence 1, Applicatio	
17	59	5.6	321	4	US-07-920-	Sequence 23, Applicati	ω.
18	59	5.6	321	0	US-08-314-	Sequence 23, Applicati	3.06e-26
19	59	5.6	597	6	US-08-187-	Sequence 2, Applicatio	

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Application UNIVERSEL FORM:  PALORMATION:  ANTION:  CANT: M.Feldmann, COANT: M.Feldmann, OF INVENTION: Ne OF	) i t		STANDARD;		1040	2444	7218 2248 2248 2248 2248 633 4810 4810 4810 4810 4810 5125 5125 5125 5125 5323 5323 5323 7218
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Sequence 24, Application US/08050319B.  CC Sequence 24, Application US/08050319B.  CC Patent(No. 5633145  CC GENERAL LEGERMATION:  CC APPLICANT: M.Feldmann, P.W. Gray, APPLICANT: M.Feldmann, P.W. Gray, CC APPLICANT: M.Feldmann, P.W. Gray, CC APPLICANT: M.Feldmann, P.W. Gray, CC TITLE OF INVENTION: Mecrosis Factor CC CORRESPONDENCE ADDRESS: CC CORRESPONDENCE ADDRESS: CC CONTENT: G35 Bryant Street CC CONTENT: G35 Bryant Street CC CONTENT: G35 Bryant Street CC CONTENT: CAlifornia CC CONTENT: G430 Bryant Street CC COMPUTER: LEM PC Compatible CC COMPUTER: LEM PC COMpatible CC COMPUTER: LEM PC COMpatible CC COMPUTER: DATE: 10-May-1993 CC CAPPLICATION NUMBER: US/08/050,319) CC APPLICATION NUMBER: US/08/050,319) CC APPLICATION NUMBER: 33,208 CC APPLICATION NUMBER: 33,208 CC RESERENCE/DOCKET NUMBER: 5150-003 CC RESTRANCE NUMBER: 33,208 CC RESTRANCE ON NUMBER: 5150-003 CC RESTRANCE ON	9050310		DNA; UNC;	ALIGNMENT	US-08-471 PCT-US95- PCT-US95-	PCT-US95- PCT-US95- PCT-US95-	US-08-232- US-08-750- US-08-636- US-08-636- US-08-369- US-08-389- US-08-189- PCT-US93-0 PCT-US93-0 PCT-US93-0 PCT-US93-0 US-08-453- US-08-238- US-08-238- US-08-238-
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Best Local Similarity 99.8%;
Matches 425; Conservative
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LOCATION: 155..1519
Sequence 2062 BP; 429 A; 617 C;
                                                                                                                                                                                                                                                                                US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP
                                                                                                                                                   GENERAL I
                                                                                                                                                                         Sequence
                                                                                                                                                                                                 Sequence 1, Application US/08321668
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                                    APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TWF RECEPTORS, THEIR PREPARATION AND
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA FEATURE:
                                                                                                                                                                                                                                                                                                                                TCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
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STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
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                               STREET:
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                                                                                                                                                  INFORMATION:
        Washington : D.C.
                                                                                                                                                              Application US/08321668 5665859
                             E: BROWDY AND NEIMARK 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double
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Pred. No. 0.00e+00;
0; Mismatches 1;
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                               Suite
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RESULT 3 ID US-08-286-740-2 STANDARD;

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Best Local Similarity 99.8%;
Matches 425; Conservative
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEFX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321/668
FILING DATE: 12-OCT-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: II 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25 618
PRESENCE /DOCKET NUMBER: 25 618
PRESENCE /DOCKET NUMBER: 35 618
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 256..1620
Sequence 2175 BP; 474 A;
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MOLECULE TYPE:
FEATURE:
TCCTGT
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                                                          TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
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                                              TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                          CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2175 base pairs TYPE: nucleic acid STRANDEDNESS: single
                      801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                               641 C; 604 G; 456 T;
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Pred. No. 0.00e+00;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                            0 other
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Best Local 9
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TELEPHONE: 415/225-1994
TELEPAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
                                                                                                                                                 1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
                                                                                                                                                                                                                                                                           STRANDEDNESS: double
TOPOLOGY: linear
Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;
            1965 CGGGACACCGTGTGTGCGCTGCAGGAAGACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                  1845
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                                                                                                                                                                                                                                             Local Similarity 99.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California
CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                        TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
                                                                                                                                      AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                    GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC
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                                                       AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                             LENGTH: 6889 bases
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                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                  425;
                                                                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                 Score 424; DB 6;
Pred. No. 0.00e+00;
0; Mismatches 1
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Best Local S
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1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
                                                                                           Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9509576
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                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764
                                                               Local
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: patin (Genericch) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                  TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGT 2150
                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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TELEPHONE: 415/952-9881
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                                                                                                                                                                                                             REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                  LENGTH: 6889 bases
                                                    40.4%;
1 Similarity 99.8%;
425; Conservation
                                                                                                                                                                                                                                                                                                                                                                94080
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                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INC
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                                                       Score 424; DB 14; Length 6889; Pred. No. 0.00e+00; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                            360 Kb floppy disk
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBDINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECHONUS: (415) 617-8999
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2145
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Patent No. 5
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                                                                                                                                                                                    STREET: 635 BIYAND CITY: Palo Alto STATE: California COUNTRY: USA ZIP: 94301
                                                                                                                                                                                                                                          APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
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                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                       Application US/08050319B
                                                                                                                                                                                                                            E: Reed & Robbins
635 Bryant Street
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                                                                         Sequence 56, Application US/08050319B
Patent No. 5633145
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
                                                                                                                                                                             Sequence 56, Application US/08050319B
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                              ADDRESSEE: Reed & 1
STREET: 635 Bryant
CITY: Palo Alto
STATE: California
                              COUNTRY:
ZIP: 943
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504 먥

635 Bryant Street

Receptor

USA

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Query Match 40.0%;
Best Local Similarity 99.3%;
Matches 423; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GATAGTGTGTGTCCCACAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mR
FEATURE:
FEATURE: CDS
LOCATION: 1.597
LOCATION: 1.597
equence 600 BP; 148 A; 157 C
                                         TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                                                                                                 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
TCCTGT 546
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                                                                                                                                                                                                                                                                                                                                                                                                  TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACATGCCTC
                                                                                  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                                                                                                                                                            AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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Pred. No. 0.00e+00;
0; Mismatches 3
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Best Local !
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                          Sequence 1, Application Patent No. 5633145
                                                                                                               US-08-050-319B-1
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 504 BP; 122 A; 137
                                                   Sequence 1, Application
                                                                     01-JAN-1900
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.I
APPLICANT: M.J.C. Turner,
                                                                                                                                                                                                                                                                                                                       404
                                                                                                                                                                                                                                                                                                                                                      344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                704
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APPLICATION NUMBER: US/08/
FILING DATE: 10-May-193
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RODDINS, RODERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                  TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                                                                                              AAACAGAACACCGTGTGCACCTG 503
                                                                                                                                                                                                                                                                                                                    AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                                                                                      AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                               TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                                                                                CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                         CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                            AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCCTTGCACAGTGGAC
                                                                                                                                                                                                                                                  AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                          382;
                                                                                                                                                                                                                                                                                                                                                                                                h 36.3%;
Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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1..501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                             STANDARD; DNA; UNC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                  US/08050319B
                                                   US/08050319B
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Pred. No. 1.31e-290;
0; Mismatches 1;
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 Brennan
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Best Local S
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US-08-050-319B-3 STANDARD; DNA; UNC; 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94301
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ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 3108
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1..501
Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GATAGTGTGTGCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
                   481 AAACAGAACACCGTGTGCACC 501
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: FEATURE:
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                                                                                                                                               CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                                                                       TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                                             TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 635 Bryant
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                             AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10
CLASSIFICATION:
AAACAGAACACCGTGTGCACC
                                                                         TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                                                                                                                                   AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/050,319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 36.1%;
Similarity 99.7%;
380; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 379; DB 7; L
Pred. No. 6.34e-289;
0; Mismatches 1;
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Best Local :
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS: ROBERTALL.
REGISTRATION NUMBER: 33.08
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                   LOCATION: 1..372
Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5633145
GENERAL INFORMATION:
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 241
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                                                                                       121 GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 180
                                                                                                                               410
                                                                                                                                                                                  350
                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         61 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 120
                                                                                                                                                                                                                                               Match 35.3%;
Local Similarity 99.7%;
                                                                                                                                                                                            1 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                              GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACCAAGTGC 409
                                                                                                                           CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG
                                                                                                                                                                                                                                                                                                  NAME/KEY:
ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG
                                               TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC
                                                                         GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC
                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
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    Application

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                                                                                                                                                                                                                                                                                                             CDS
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                                                                                                                                                                                                                                             Score 370; DB 7; L
Pred. No. 2.44e-281;
                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                   1; Indels
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Best Local S
Matches 30
                                                                                                                                        Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 49, Application US/08050319B Patent No. 5633145
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                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, vers
SOFTWARE: PATENTIN Release #1.0, vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBETTA L.
NAME: ROBBINS, ROBETTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49, Application US/08050319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650
165 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 224
                          454 GGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAG 513
                                                     105 GGACAGGGAGAGAGAGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAG 164
                                                                                                                                                                                                                                                                                     TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 AACACCGTGTGC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
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                                                                          Local Similarity 97.8%;
les 309; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710 AACACCGTGTGC 721
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107-8999
TELECOMMUNICATION 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 9430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                       474 base pairs
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635 Bryant Street
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Pred. No. 3.55e-224;
Predematches 7;
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                                                                                                             Length 474;
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                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEPAX: (404) 815-6555
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2771 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Falk, Per APPLICANT: Gordon, Jeffrey I. TITLE OF INVENTION: Animal Model for Gastro-Intestinal TITLE OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                   MOLECULE TYPE: UN
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                               PUBLICATION INFORMATION:
                                                     HYPOTHETICAL:
ANTI-SENSE: 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Sweetser, et al
Genes & Dev.
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                                                                                    DNA (genomic)
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Best Local :
                                                                                                                                                        Patent No. 500111.
GENERAL INFORMATION:
GENERAL INF
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                                                                                                                                                                                                             Sequence 3, Application US/08343401A Patent No. 5661132
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                                                                                                                                                                                                                                                              Sequence 3, Application US/08343401A
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                                                                                    APPLICANT: Swain, William F
APPLICANT: Macklin, Michael D
APPLICANT: Eriksson, Elof
APPLICANT: Andree, Christophe
TITLE OF INVENTION: Improved Wo
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
AUTHORS: Sweetser, et al
JOURNAL: J. Biol. Chem.
VOLUME: 261
PAGES: 5553-5561
DATE: 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 28.6%;
Local Similarity 97.3%;
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                                                                   CORRESPONDENCE ADDRESS:
STREET:
CITY: M
STATE:
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DATE: 1982
RELEVANT RESIDUES IN SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLUME: 2
PAGES: 1318-1332
DATE: 1988
RELEVANT RESIDUES IN SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTGCTCTGCCTGCCTTGCAAGAGGGCAGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCTCTGTTGCCCTCTGGTTTCTCCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG
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                                                 ADDRESSEE:
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 Madison
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                                  PO Box 2113
                                                   Quarles & Brady
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Pred. No. 1.69e-222;
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Best Local Similarity 96.2%;
Matches 326; Conservative
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4283 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP
                                              NAME/KEY: sig_peptide
LOCATION: 713..1049
Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: pWRG1630
                                                                                                           CTCCCTCTGTTGCCCCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCCTCCTGGCTTTT
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LOCATION:
                                                                                                                                                              TGGAGAGAGAAAACAAACAAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCCGG
                                                                                                                                                                                            TATCGCCATGTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTC-CTCCCTGGAGGGA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/O: FILING DATE: 22-NOV-1994 CLASSIFICATION: 514
                                                                                                CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTT
                                                                                                                                               TGGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGAGAGTGCTGGCCTCTTGCTCTCCGG
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4283 base pairs
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Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
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GENERAL INFORMATION:
APPLICANT: Erikss
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                                                                   891 TGGAGAGAGAAAAACAACAGCTCCTGGAGCAGGGAGAGTGTTGGGCCTCTTGCTCCGG
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                                                                                                                                                              66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGGCTTCTCAATCTCAC
                                                                                                                                                                                                                                                                        y Match 28.4%;
Local Similarity 96.2%;
hes 326; Conservative
                                                                                                                                                                                                                   6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAAGAGG
                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: joir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Plasmid DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/445,265A FILING DATE: CLASSIFICATION: 604
CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTT
                                                    TGGAGAGAGAAAAACAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4283 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 53703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Quarles & Brady STREET: 1 South Pinckney S
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Pred. No. 8.01e-221;
0; Mismatches 10;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Mecrosis Factor alpha) Receptor
TITLE OF SPOHENCES: 57
                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 1..474
Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53, Application US/08050319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1900
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                                            344
                                                                                                         121 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTTGCTGTACC 180
                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                           y Match 24.3%;
Local Similarity 98.9%;
hes 258; Conservative
                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                           MOLECULE TYPE:
TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
            TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
                                                                                            GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATAATTCCATTTGCTGTACC 403
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 635 Brya
CITY: Palo Alto
STATE: Californ:
                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 Bryant Street
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                                                                                                                                                                                                                                           cDNA to mRNA
                                                                                                                                          Score 255; DB 7; Le
Pred. No. 7.22e-185;
0; Mismatches 3;
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                                                                                                                                                                  Length 477
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                                                                                Matches
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Best Local
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
                                                                                                                           NAME/KEY: CDS
LOCATION: 1..459
Sequence 462 BP; 116 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JT 14
US-08-050-319B-51 STANDARD; DNA; UNC; 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/08050319B
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APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Negrosis Factor alpha) Receptor
300 CAGCCTCTGCCTCAATGGGACCGTGCACCTCCTCCTGCCAGGAGAAACAGAACACGTGTG
                                    601 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584
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                                                         240 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 299
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415):617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                               FEATURE:
                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGGACACCGTGTGTACCTGC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01
FILING DATE: 10-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
                                                                                                                                                                                      TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 6
                                                                                169;
                                                                                          16.1%;
Similarity 100.0%;
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                                                                               Conservative
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635 Bryant Street
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                                                                                                                                                                                                 double
                                                                                                                            A; 119 C; 121 G; 106 T; 0 other;
                                                                                                                                                                                                                                                       327-3231
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                                                                                          Score 169; DB 7; L
Pred. No. 1.18e-113;
                                                                                0; Mismatches
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                                                                                0;
                                                                                                     Length 462;
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             359
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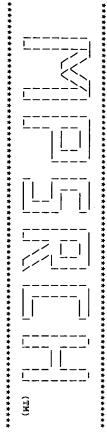
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661 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG

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Matches
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                                                                                                                                                                                                                                                                                MOLECULE TYPE: cDNA
Sequence 534 BP; 108 A; 166 C; 143 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08187756C Patent No. 5597709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08187756C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-187-756C-3 STANDARD; DNA; UNC; 534 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,756C
FILING DATE: January 27, 1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION TOMBER:
FILING DATE:
APPLICATION TOMBER:
APPLICATION T
  333
                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         721 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGT 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 CACCIGCCATGCAGGITTCTTTCTAAGAGAAAACGAGIGIGICTCCCIGT 408
                                             68 AGGGCAGTGCC 78
                                                                                                                                                                                         Match 6.6%;
Local Similarity 98.6%;
les 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36.134
REFERENCE/DOCKET NUMBER: 325800-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROSEN, ET AL.
TITLE OF INVENTION: Human Growth Hormone
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
AGGGCAGTGCC 343
                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6 BECKER F
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                         Score 69; DB 6; Lo
Pred. No. 9.14e-34;
0; Mismatches 1
                                                                                                                                                                                                                                         Length 534;
                                                                                                                                                                                            1;
                                                                                                                                                                                            Indels
                                                                                                                                                                                            0
                                                                                                                                                                                         Gaps
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Search completed: Wed May 6 10:02:47 1998

Job time : 122 secs



Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Wed May 6 08:27:00 1998; MasPar time 4.88 Seconds 394.142 Million cell updates/sec

Tabular output not generated.

>US-08-804-166-8 (1-336) from US08804166.pep 2541

Description: Perfect Score: Sequence: 1 SRTSLLLAFGLLCLPWLQEG......PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150 Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 30.838; Variance 140.153; scale 0.220

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

11111111111111111111111111111111111111	Result
1322 1242 1025 1025 1025 1025 1020 995 996 996 996 714 714 666 661 651 339	Score
52.0 40.3 39.2 23.0 28.1 12.3 3.5 3.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2	Query Match
455 1455 1455 1455 1457 1457 1457 1457 1	Length
777766766677776766777	BB
US-08-321 US-08-050 US-08-425 US-08-425 US-08-425 US-08-050 US-08-050 US-08-050 US-08-050 US-08-050 US-08-050 US-08-425	ID
Sequence 25 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 11 Sequence 21 Sequence 21 Sequence 21 Sequence 21 Sequence 11 Sequence 11 Sequence 12 Sequence 12 Sequence 12 Sequence 12 Sequence 12 Sequence 12 Sequence 13 Sequence 12 Sequence 13 Sequence 14 Sequence 15 Sequence 15 Sequence 16 Sequence 17 Sequence 17 Sequence 18 Sequence 19 Sequence 19 Sequence 19 Sequence 10 Sequence 10 Sequence 10 Sequence 11	Description
Applicatio	! ! ! ! ! !
1.11e-110 1.11e-110 2.75e-103 6.14e-83 1.79e-82 3.81e-80 3.07e-80 3.07e-80 3.07e-80 7.64e-74 1.64e-74 1.64e-74 1.74e-56 4.01e-56 4.01e-54 5.77e-56 4.01e-54 5.77e-48 7.49e-48 7.49e-48 4.04e-49 3.84e-24 3.84e-24 3.84e-24 3.84e-24	Pred. No.

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23
209	212	210	212	221	221	225	225	227	227	227	227	230	249	249	260	261	268	282	287	287	296	298
8.2	8.3	8.3	8.3	8.7	8.7	8.9	8.9	8.9	8.9	8.9	8.9	9.1	9.8	9.8	10.2	10.3	10.5	11.1	11.3	11.3	11.6	11.7
		355										41								111		39
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5451527-5	5395760-4	US-08-292-	US-08-086-	PCT-US91-0	US-08-292-	PCT-US91-0	US-08-292-	PCT-US94-0	5451527-12	5451527-8	5451527-4	us-08-086-	US-08-086-	us-08-086-	5177193-3	us-08-086-	US-08-086-	US-08-425-	US-08-425-	US-08-425-	5451527-1	US-03-050-
Patent No. 5451527.		6, P	ь	Sequence 4, Applicatio	4	2	2,	Sequence 29, Applicati	Patent No. 5451527.	Patent No. 5451527.		Н	13,	ŗ	o. 51	12,	14,	δ	ω	Sequence 4, Applicatio	Patent No. 5451527.	Sequence 40, Applicati
6.52e-09	. 65e	.38e	3.65e-09		. 38e	.93e-1	.93e-	1.98e-10	÷		1.98e-10	1.10e-10	2.65e-12	. 65e		2.47e-13	6.14e-14	.77e-	.39e-	1.39e-15	28e-	1.53e-16

# ALIGNMENTS

88888888	188888888888888	388888888888888	RESULT TO UT
ATTORNEY/AGENT INFORMATION:  NAME: BROWDY, ROGER L.  REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: WALLACH=13 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-638-5197 TELEPHONE: 202-638-5197 TELEFAX: 202-737-3528 TELEX: 248633	ZIP: 20004  CIP: 20004  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOPTWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/08/321,668  FILING DATE: 12-OCT-1994  CLASSIFICATION: 435  PRIOR APPLICATION DATA:  APPLICATION NUMBER: IL 107268  FILING DATE: 12-OCT-1993	PATENT NO. 565859  GENERAL INFORMATION: APPLICANT: WALLACH, David APPLICANT: WALLACH, David APPLICANT: WALFOLOMEEV, Eugene APPLICANT: BATKIN, Michael TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF TITLE OF INVENTION: THE THE THE RECEPTORS, THEIR PREPARATION AND THEIR USE NUMBER OF SEQUENCES: ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C.	S-08-321-668-2 STANI xxxxx  1-JAN-1900 equence 2, Application (

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  SEQUENCE
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                                                                                              CONFUTER READABLE FORM:

MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RODDINS, RODERTA L.
REGISTRATION NUMBER: 3508
REFERENCE/DOCKET NUMBER: 3500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
                                                TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Local Similarity 100.0%;
es 171; Conservative
MOLECULE TYPE: protein
JENCE 455 AA; 50579 MW; 1048388 CN;
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Modified human TNFalpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 455 AA; 50494 MW; 1048031 CN;
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STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
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                                   TYPE: amino acid
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Best Local S
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Best Local S
Matches 15
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NAME: ROBBINS, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

REFERENCE/COKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 199 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 199 AA; 22186 MW; 195553 CN;
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                                                                                                            SEQUENCE
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Local Similarity 100.0%;
les 171; Conservation
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              41 DSVCPTGKYIHPONNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435
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STATE: California
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                                                                    Similarity
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                                                   Score 1243; DB 7;
Pred. No. 2.75e-103;
0; Mismatches 1;
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Pred. No. 1.11e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
TITLE OF INVENTION: Methods For Preparing and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                67
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TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/7
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUCCIDO, Richard R.
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                               HYPOTHETICAL: NO
ANTI-SENSE: NO
JENCE 145 AA; 15544 MW; 114662 CN;
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                    TOPOLOGY: 11
MOLECULE TYPE:
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                                   NUMBER OF SEQUENCES:
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IRLPGCPRGVNPVVSYAVALSCQCALCRRSTIDCGGPKDHPLICDDPRFQDSSSSKAPPP 126
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                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                            TYPE: amino acid
                                                                                   ch 40.3%;
l Similarity 99.3%;
l38; Conservative
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                                                                                   Score 1025; DB 6;
Pred. No. 6.14e-83;
0; Mismatches 1
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                                                                                  Query Match 40.3%;
Best Local Similarity 99.3%;
Matches 138; Conservative
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                                                                                                                              SEQUENCE
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                      67
                                                                                                                                                                                         TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEGGTH: 145 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,5
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                       ANTI-SENSE:
                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
            IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
                                       IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP
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CITY: Princeton
                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                TYPE: amino acid
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    Robert K.
Analogs of Glycoprotein Hormones Having
Altered Receptor Binding Specificity and
Methods For Preparing and Using Same

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Pred. No. 6.14e-83;
0; Mismatches 1; Indels
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DSI1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-638-3939 or 803-272-1471
TELEFAX: 919-638-3939 or 803-272-1471
INFORMATION FOR SEQ ID NO: 1:
7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
                                                                                                                        IDENTIFICATION METHOD: N-te
PUBLICATION INFORMATION:
AUTHORS: Keutmann et alia
TITLE: "A Receptor binding
JOURNAL: Proc Nat'l Acad Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: Microsoft World 7.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dr. Laurence A. Cole and Dr. Andrew Kardana TITLE OF INVENTION: No. 5674727el Methods for Detecting Reproductive TITLE OF INVENTION: Cancers or Tumors and Assay Products TITLE OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Brian D. Voyce
REGISTRATION NUMBER: 28,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       ORIGINAL SOURCE: FEATURE:
                                                                                                                                                                                                                            MOLECULE TYPE: subunit of hormone, MOLECULE TYPE: beta\subunit of hCG
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 08/31/94 CLASSIFICATION: 435
                                                                               DATE:
                                                                                PAGES: 2038-2042
DATE: 1987
                                                                                                      ISSUE:
                                                                                                                VOLUME:
                                                                                                                                                                                 NAME/KEY: beta subunit of hCG that is nicked by GBNE LOCATION: hCG
                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                        l Similarity
137; Conser
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                                                                    145 AA; 15476 MW; 116769 CN;
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                                                                                                  5674727 applicable
                                  40.1%;
98.6%;
                                                                                                                                                                                                                                                              No. 5674727 applicable
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                                                                                                                                                                                                                  human urine
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                                  Score 1020;
Pred. No. 1
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 198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
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                                                     Match 39.2%;
Local Similarity 96.4%;
                                                                                                                                                                                 TELEFAX: (609) 466-2760 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07,
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUCCLIO, Richard R.
REGISTRATION NUMBER: 32,5;
           7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
                                                                                    HYPOTHETICAL: NO
ANTI-SENSE: NO
JENCE 145 AA; 15448 MW; 114931 CN;
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acid
TYPE: amino acid
                                                                                                                                                                                                        TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Analogs of Glycoprotein Hormones Havi
TITLE OF INVENTION: Altered Receptor Binding Specificity
TITLE OF INVENTION: Methods For Preparing and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Moyle, Wil
APPLICANT: Campbell,
                                                                                                                          MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: UMD 1.0-004
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New Jersey
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                                                                                                                                                            145 amino acids
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                                                                                                                : peptide
NO
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                                                     Score 995; DB 6;
Pred. No. 3.81e-80;
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REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3331
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57, Application US/08050319B
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                                                                                                            SEQUENCE
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143
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GENERAL INFORMATION:
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                                                    83
                                                                                                                                                                                                 SOFTWARE: Patentin Release CURRENT APPLICATION NUMBER: US/08/
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                             STREET: DIALTO CITY: Palo Alto CITY: California
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Modified human TNFalpha (Tumor TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                          APPLICANT: M.Feldmann, P.V
APPLICANT: M.J.C. Turner,
                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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       KQNTVCT 167
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                                                                                                                        TYPE: ami
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                                                                                39.2%;
l Similarity 100.0%;
l27; Conservative
                                                                                                           167 AA; 18626 MW; 139513 CN;
                                                                                                                                                                                                                                                                         94301
                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                635 Bryant Street
                                                                                                                                                                                                                                                                                                                                           M.Feldmann, P.W. Gray, M.J.C. Turner, F.M Brennan
                                                                                                                                                                                                                                     PatentIn Release #1.0, version #1.25
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                                                                                Pred.
                                                                                       Score 996; DB 7;
Pred. No. 3.07e-80;
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                                                                                Mismatches
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REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEFAX: (415) 327-3331
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE 167 AA; 18626 MW; 139513 CN;
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US-08-050-319B-4
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                                                                    143
                                                                                                                                                       101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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                                                                                                 161 KQNTVCT 167
                                                                                                                                       83
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                                                                                                                                                                                                       23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,2
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COMPUTER READABLE FORM:
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l Similarity 100.0%;
127; Conservative
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STANDARD;
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Pred. No. 3.07e-80;
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                                           Sequence 50, Patent No. 50
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Patent No.
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                              GENERAL INFORMATION:
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Local Similarity 100.0%;
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    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
UNMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: ROBEITS L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acid
                                                                                                                                                                                                                              NTVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                   SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYMSENLFQCFNCSLCLNGTVHLSCQEKQ 144
                                                                                                                                                                                                                                                                                                                                         VCPQGKTIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
                                                                                                                                                                                                                                                                                                              SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: ami
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 10-May-1993 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LE TYPE: protein
124 AA; 14047 MW;
                                           ), Application 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H: 124 amino acids
amino acid
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  M.Feldmann, P.W. Gray,
M.J.C. Turner, F.M Brennan
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                                                                                                                                                                        STANDARD;
                                                          US/08050319B
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Pred. No. 7.64e-79;
0; Mismatches 0;
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Best Local S
Matches 11
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MOLECULE TYPE: protein
SEQUENCE 157 AA; 17570 MW; 122247 CN;
                                                                                                                                                                                               Sequence 9, Application US/08425673.
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-Msy-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      Patent No.
                                                                                                                                                                   Sequence 9, Application US/08425673
                                                                                                                                                                                                                                                                                                                                         180 QI 181
                                                                                                                                                                                                                                                                                                                                                                   156 QI 157
                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 36.5%;
Local Similarity 97.5%;
les 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS
                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
                                                                 TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having TITLE OF INVENTION: Altered Receptor Binding Specificity an TITLE OF INVENTION: Methods For Preparing and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
                                        CORRESPONDENCE ADDRESS
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                                                                                                             APPLICANT:
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                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 179
 STREET:
CITY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 635 Bryant Street CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Robbins, Roberta L. REGISTRATION NUMBER: 33,208
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                           ADDRESSEE:
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Princeton
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             E: Richard R. Muccino
P.O. Box 1267
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                                                                                                            Campbell, Robert K
                                                                                                                          Moyle,
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                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                          William R.
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Pred. No. 6.44e-74
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    Mismatches

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                                                                                 Specificity and Activity and
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Gaps 95

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COUNTRY:

USA

New Jersey

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Best Local :
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                                                                                                                                                                                           Sequence 7, Application US/08425673 Patent No. 5508261
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity
TITLE OF INVENTION: Methods For Preparing and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (609) 466-2760 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                             7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                          STREET: F.C.
STREET: Princeton
CITY: Princeton
CTATE: New Jersey
HSA
                                                                                       NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
                                   COUNTRY:
ZIP: 085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Muccino, Richard REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/425,673 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%;
Similarity 93.3%;
97; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 AA; 12250 MW; 68564 CN;
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                                                                        P.O. Box 1267
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Pred. No. 1.61e-56;
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Best Local :
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08425673.
                                                                                                                                                                                                                                                                                                                                                             XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 305
                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Moyle,
APPLICANT: Campbe
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Local Similarity 91.7%;
hes 99; Conservative
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                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                   APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity an
TITLE OF INVENTION: Methods For Preparing and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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SOFTWARE: Patentl
                                                                                                                  COUNTRY:
                                                                                                                              STATE:
                                                                                                                                           CITY:
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                      APPLICATION NUMBER:
                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                          Princeton
                                                                                                         08551
                                                                                                                             New Jersey
                                                                                                                                                P.O. Box 1267
                                                                                                                  USA
                                                                                                                                                                                                                                                  Moyle, William R.
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514
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                      US/08/425,673
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Pred. No. 5.77e-56;
0; Mismatches 9
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Best Local Similarity 98.9%;
Matches 93; Conservative
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SEQUENCE 117 AA; 12890 MW; 72412 CN;
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                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08425673.
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                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pepti
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,673
                                                                                                                                                                                                                                                      APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
TITLE OF INVENTION: Methods For Preparing and Using Same
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/717,151
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. Box
CITY: Princeton
STATE: New Jersey
  REGISTRATION NUMBER: 32,538
                                                                   CLASSIFICATION: 514
                                                                              FILING DATE:
                                                                                                                                                                     ZIP: 08551
                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                              E: Richard R. Muccino
P.O. Box 1267
                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 714; DB 6;
Pred. No. 4.01e-54;
0; Mismatches ]
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Best Local S
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258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC
                                              198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
             67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDC 100
                                                                                                                                                                                                                                                  TELEFAX: (609) 466-2760 INFORMATION FOR SEQ ID NO:
                                                             7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pepti
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acid
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UM TELECOMMUNICATION INFORMATION: TELEPHONE: (609) 466-3407
                                                                                           26.9%;
l Similarity 94.7%;
89; Conserva+1...
                                                                                                                                                114 AA; 12242 MW; 69571 CN;
                                                                                                                                                                                                                         114 amino acids
                                                                                                                                                                                      peptide
                                                                                                            Score 684; DB 6;
Pred. No. 2.31e-51;

    Mismatches

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291
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                                                                                                                      Length 114;
                                                                                               Indels
                                                                                               0
                                                                                               Gaps
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0

TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids

pept1de

REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD 1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407

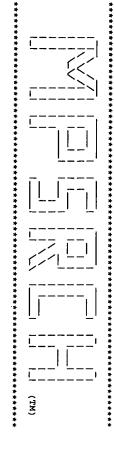
.0-004

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:

US 07/717,151

NAME: Muccino, Richard R.

Search co completed: Wed May ne : 26 secs. 6 08:27:26 1998



Release 3.0.5AA John F. Collins, Biocomputing Research Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd Unit.

MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Tabular output Run on: not generated. Wed May 6 11:17:48 1998; MasPar time 73.35 Seconds 934.882 Million cell updates/sec

Title: >US-08-804-166-7

Description:
Perfect Score:
N.A. Sequence: 1301 (1-1301) from US08804166.seg 1 CTCGAGATGGCTACAGGTAA.....

Comp: CTCGAGATGGCTACAGGTAA......CACAATAAGGATCCCTCGAGGAGCTCTACCGATGTCCATT......GTGTTATTCCTAGGGAGCTC

1301

Scoring table: TABLE default Gap 6

Nmatch

Searched: 102136 seqs, 26354296 bases x 2

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

n-issued 1:back 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Database:

Statistics: Mean 8.845; Variance 4.678; scale 1.891

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5.3	5.3	6.5	7.6	7.9	17.0	19.8	23.3	23.3			28.6								Query Match
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Sequence 1	Sequence 3	Sequence 1	Sequence 1	Sequence 2	Sequence 5:	Sequence 53	Sequence 1	Sequence 3,	Sequence 5,	Sequence 49	Sequence 3,	Sequence 1,	Sequence 56	Sequence 4	Sequence 2,	Sequence 2,	Sequence 1,	Sequence 24	Description
Applicatio	Applicatio	1, Applicati	, Applicatio	, Applicatio	l, Applicati	3, Applicati	, Applicatio	, Applicatio	, Applicatio	•	Applicatio	, Applicatio	5, Applicati	7, Applicati	, Applicatio	Applicatio	Applicatio	i, Applicati	
9.66e-32	9.66e-32	1.00e-42	6.30e-54	6.08e-57	1.21e-148	3.56e-177	7.97e-214	7.97e-214	1.27e-214	1.22e-254	4.39e-269	2.60e-276	6.44e-278	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	Pred. No.

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	ALIGNMENTS	US-08-273-	us-07-865-	PCT-US95-1	US-08-050-	US-08-239-	US-08-238-	5177193-2	PCT-US93-0	US-08-453-	US-08-453-	PCT-US93-0	US-08-188-	PCT-US95-0	PCT-US93-0	PCT-US94-0	US-08-453-	US-08-388-	US-08-232-	US-08-238-	US-08-475-	US-08-369-	US-08-780-	90-	-8	-08-3	us-07-920-	
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US-08-050-319B-24 STANDARD; DNA; UNC; 2062 BP

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01-JAN-1900

Sequence 24, Application US/08050319B

Sequence 24, Application US/08050319B Patent No. 5633145 GENERAL INFORMATION:

NUMBER OF SEQUENCES: 5 APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor

STREET: 635 Bryant CITY: Palo Alto STATE: California COUNTRY: ADDRESSEE: 635 Bryant Street USA Reed & Robbins

ZIP: 94301 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA: Floppy disk version #1.25

ATTORNEY/AGENT INFORMATION:
NAME: ROBEITS, ROBEITS,
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 51: APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435 5150-0030

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:

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Patent No.
                                                                                                         Sequence 1, Application
                                                                                                                         01-JAN-1900
                                                                                                                                                                  US-08-321-668-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
            GENERAL INFORMATION:

APPLICANT: WALLACH, David

APPLICANT: BRAKEBUSCH, Cord

APPLICANT: VARFOLOMEEV, Eugene

APPLICANT: VARFOLOMEEV, Eugene

APPLICANT: WALLACH, MICHAEl

TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING

TITLE OF INVENTION: THE THE RECEPTORS, THEIR PREPARATION

NUMBER OF SEQUENCES: 42

CORDESCENTENCE ALDEREG:
                                                                                                                                                                                                                                                                                                                                                                                                                                    405
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FEATURE:
NAME/KEY: CDS
LOCATION: 155..1519
Juence 2062 BP; 429 A; 617 C;
        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                          AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                          N
                                                                                                                                                                                                 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG
                                                                                                                                                                                                                                  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCCAGATTGAG
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Similarity 100.0%;
514; Conservative
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                                                                                  , Application 5665859
                                                                                                                                                                  STANDARD; DNA; UNC; 2175
BROWDY AND NEIMARK
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                                                                                                         US/08321668
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Matches 514;
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TELEFAX: 24863
INFORMATION FOR SEQUENCE CHARACTERS

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEFAX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
Sequence 2175 BP; 474 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 12-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,6
                                                                                                                                                         TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                     TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
                                                                                                                                                                                                                                                              CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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                                                                                                                   CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
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Similarity 100.0%;
514; Conservative
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Pred. No. 0.00e+00;
0; Mismatches (
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Best Local :
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REFERENCE/DOCKET NUMBER: 798
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEPAS: 415/952-9881
TELEERS: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
                                                                                                       STRANDEDNESS: double
TOPOLOGY: linear
Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;
                         1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
                                                                       1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KI
MEDIUM TYPE: 5.25 inch, 360 KI
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DI
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08286740
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                                                                                                                                                                     Local
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Crowley, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
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CITY: South San Francisco
STATE: California
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            TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                           AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                          LENGTH: 6889 bases
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                                                                                                                                                         39.5%;
1 Similarity 100.0%;
514; Conservative
                                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                    Score 514; DB 6;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 Kb floppy disk
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       NAME: Lee, Wendy M.

REGISTRATION NUMBER: 798E
REFERENCE/DOCKET NUMBER: 798E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/925-1994
TELEPAX: 415/952-9881
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6889 bases
TYPE: nucleic acid
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                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                        FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCCTACCCCCAGATTGAG 2204
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                                                                                                                                                     APPLICATION NUMBER: 08/2
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CITY: South San Francisco
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VENTION: METHOD FOR
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Best Local
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Patent No. 5
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                                                                                                                 APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Recepto:
NUMBER OF SEQUENCES: 57
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                        NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
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STATE: California
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ince 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;
                                             ZIP: 94301
                                                      COUNTRY:
                                                                                     STREET:
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                                                                                     E: Reed & Robbins
635 Bryant Street
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Sequence 56,

Application US/08050319B

01-JAN-1900

Sequence 56, Application US/08050319B Patent No. 5633145

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Matches 477; Conservation
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SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..597
Sequence 600 BP; 148 A; 157 C; 162
US-08-050-319B-56
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NAME: ROBEITS. ROBEITS.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, version CURRENT APPLICATION DATA:
                                                         TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCCAGATTTAG
            σ
                                                                                                      AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTTCTTAGAGAGAAAACGAGTGTGTCT
                                                                                                                                    CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                                                         TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 10-May-1993 CLASSIFICATION: 435
                                             TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
                                                                                          CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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STANDARD;
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Pred. No. 0.00e+00;
0; Mismatches 3
DNA;
UNC;
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Matches
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Best Local 9
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LOCATION: 1..501
Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS: LENGTH: 504 bass Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
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ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319B

FILING DATE: 10-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 29.4%;
Local Similarity 100.0%;
les 383; Conservative
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APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA FEATURE:
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ADDRESSEE: Reed & Robbins
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STREET: 635 Bryant
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                              TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
                                                                                                                                                                                                                                                                                                               AAACAGAACACCGTGTGCACCTG 503
                                              TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                             AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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                                                                                                                                                                                                Query Match 29.3%;
Best Local Similarity 100.0%;
Matches 381; Conservative
                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..501
Sequence 501 BP; 121 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-050-319B-1 STANDARD; DNA; UNC; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1900
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                        301
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                                                                                                                                                REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
FEATURE:
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FILING DATE: 10-MAY-1993
CLASSIFICATION: 4.35
ATTORNEY/AGENT INFORMATION:
NAME: ROBDINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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              AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                              TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCCACCTCAGACACTGCCTC
                                                                                                              AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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                                                                                                                                                                                                                                                  A; 137 C; 137 G; 106 T; 0 other;
                                                                                                                                                                                                Score 381; DB 7; L
Pred. No. 2.60e-276;
0; Mismatches 0;
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                            Query Match 28.6%;
Best Local Similarity 100.0%;
Matches 372; Conservative
                                                                                                                                     APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: ROBBITS ROBBITS ROBERT L. REGISTRATION NUMBER: 33,208 REFERENCE/DOCKET NUMBER: 5150-0030 TELECOMMUNICATION INFORMATION: TELEPRONE: (415) 617-8999 TELEPRAX: (415) 327-3331 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 372 base pairs
                                                                Sequence 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Patent No. 5
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APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                             FEATURE:
                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
                                                            NAME/KEY: CDS
LOCATION: 1..372
ence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 420
                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACAGAACACCGTGTGCACC 501
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STATE: California
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5633145
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                                                                                                    DNA (genomic)
                            Score 372; DB 7; Le
Pred. No. 4.39e-269;
0; Mismatches 0;
                                              Length 372;
                             Indels
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                                     TELEFAX: (415) 327-32: INFORMATION FOR SEQ ID NO:
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               SEQUENCE CHARACTERISTICS:
LENGTH: 474 base pairs
 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 AACACCGTGTGC 372
                REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCCTGCCAGGAGAAACAG
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                                                                                                                                                           APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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635 Bryant Street
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327-3231
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                                                                                                                                                                                                                                       Sequence 5, Application US/08273411 Patent No. 5625124
                                                                                                                                                                                                                                                                        Sequence 5, Application US/08273411
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                                                                                                                                                                                                                                                                                                                                                       US-08-273-411-5 STANDARD; DNA; UNC; 2771
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Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 GGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAG 514
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                                                                                                                                                                                                                           GENERAL INFORMATION:
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Local Similarity 97.8%;
ses 362; Conservative
                 COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                    APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Animal Model
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                      APPLICANT:
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LOCATION: 1..
                                                                                                           CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACC 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC
        APPLICATION NUMBER:
                                                                                                                                   STREET:
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                                                                                                           Georgia
                                                                                                                                 1100 Peachtree Street,
                                                                                                                                                                                                                 Falk, Per
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         US/08/273,411
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Pred. No. 1.22e-254
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                                                                                                                                 Suite 2800
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RESULT ID U

US-08-343-401A-3 STANDARD;

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Best Local Similarity 97.9%;
Matches 331; Conservative
                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
AUTHORS: Sweetser, et al.
JOURNAL: J. Biol. Chem.
VOLUME: 261
PAGES: 5553-5561
DATE: 1986
RELEVANT RESIDUES IN SEQ ID NO: 9
Sequence 2771 BP: 666 A; 718 C; 704 G;
                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: WU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
247
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                                                                                              856
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ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
JOURNAL:
VOLUME:
                                                                                     GGAGAGAGAAAAAAAAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC
                                                                                                                           TATCGCCATGTAAGCCCAGTAT--GGCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
JOURNAL:
VOLUME:
                                               TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG
                                                                                                                TATCGCCATGTAAGCCCAGTATTTGGCCAATGTCAGAAAGCTCCTGGTCCCTGGAGGGAT 186
                                                                           GGAGAGAAAAAACAACACCTCCTGGAGCAGGGAGAGTGCTGCCCTCTTGCTCTCCGGC
                                      TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTTGGCTTTTG
                                                                                                                                                                                                                                                                                                                                                                   PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                   DATE: 1988
RELEVANT RESIDUES IN SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub
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Genes & Dev.
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Pred. No. 1.27e-214;
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3; 683 T; 0 other;
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Best Local Similarity 95.6%;
Matches 323; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 4283 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,401A
FILING DATE: 22-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
PRESSTRUCE OF COMPANY OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                            Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
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                                                                                                          713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCCTTTGG-CACAATGTGTGCTGAGGGGAGAGGG
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                      772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
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NAME/KEY:
LOCATION:
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APPLICANT: Macklin, Michael D
APPLICANT: Eriksson, Elof
APPLICANT: Andree, Christophe
TITLE OF INVENTION: Improved Wound Healing
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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LOCATION:
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ZIP: 53701-2113
CAGCGACCTGTAGATGGGACGGGGCACTAACCCTCAGGTTTGGGGGCTTCTGAATGTGAG
                                                                                     ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG
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981..1253
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713..1049
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                                                                                                                                                                                           Score 303; DB 7; Length 4283; Pred. No. 7.97e-214;
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ID US-08-445-265A-1 STANDARD; DNA; UNC; 4283
            Query Match
Best Local
   Matches
                                                LOCATION: jo
Sequence 4283 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08445265A Patent No. 5697901
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                                                                                                                                                  TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4283 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Erikss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307
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                                                                                   MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Plasmid DNA" FEATURE:
                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,265A
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 1:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Eriksson, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCCTCTGTTGCCCTCTGGTTTCTCCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG
                                                                                                                     TOPOLOGY: circular
                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTGCTCTGCCTGCCTTGGCTTCAAGAGGGCAGTGCC 344
                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 53703
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
            1 23.3%; Similarity 95.6%;
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 South Pinckney Street
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                                            join(713..721, 981..1250)
>; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
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            Score 303; DB 7; L
Pred. No. 7.97e-214;
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  Mismatches
                       Length 4283;
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Gaps
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RESULT
ID US
                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53, Application US/08050319B Patent No. 5633145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
    MOLECULE TYPE:
                  TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTGCTCTGCCCTGCCTTCAAGAGGGCAGTGCC 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCGACCTGTAGATGGGACGGGGCACTAACCCTCAGGTTTGGGGGCTTCTGAATGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        635 Bryant Street
                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed & Robbins
    CDNA to mRNA
                                 double
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Best Local S
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GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51, Application US/08050319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                        SOFTWARE: Patentin Release #1.0, ver:
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 31,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Recepto
                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATAGTGTGTGCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGGACACCGTGTGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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                                                                                 REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                         STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                         STREET: 635 Bryant Street CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.8%;
Similarity 99.2%;
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Pred. No. 3.56e-177;

 Mismatches

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Best Local :
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                                           COMPUTER READABLE FORM:

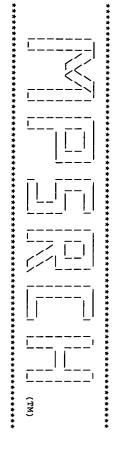
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,915
FILING DATE: 07-JUL-193
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kubovcik, Ronald J.
REFERENCE/DOCKET NUMBER: 15873005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-6300
TELEPHONE: 202-467-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5444167
GENERAL INFORMATION:
APPLICANT: Petter
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08086915 Patent No. 5444167
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08086915
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-086-915-2 STANDARD; DNA; UNC; 138
TELEFAX: 202-466-2006 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 138 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 GAAAAGCCTGGAGTGCACGAAGTTGTGCCCTACCCCAGATTTAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCCTGTAGTAACTGTAA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGGAGAACACCGTGTG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 Match 17.0%;
Local Similarity 99.6%;
les 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         APPLICANT: Pettersson, Kim SI
TITLE OF INVENTION: Variant Luteinizing Hormone Encoding DNA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                         STREET: 1140 Cont
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824
                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20036
                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                  E: Adduci, Mastriani, Schaumberg & Schill
1140 Connecticut Avenue, N.W., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 221; DB 7; Length 462; Pred. No. 1.21e-148;
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                                                                                       Query Match 7.9%;
Best Local Similarity 99.0%;
Matches 104; Conservative
                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
DEVELOPMENTAL STAGE: Adult
Sequence 138 BP; 24 A; 51 C; 42 G;
                                             870 CCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 929
Score 103; DB 5;
Pred. No. 6.08e-57;
0; Mismatches 1
                                                                                                                                   G; 21 T; 0 other;
                                                                                         1;
                                                                                                             Length 138
                                                                                         Indels
                                                                                         0
                                                                                         Gaps
                                                                    93
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Search completed: Wed May 6 11:19:13 1998 Job time: 85 secs.



Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Run on: Wed May 6 08:23:57 1998; MasPar time 4.43 Seconds 368.292 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-6

Description: (1-285) from US08804166.pep
Perfect Score: 2183

Sequence: 1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTACHCSTCYYH

Perfect Score: 2183
Sequence: 1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTACHCSTCYYHKS 285
Scoring table: PAM 150
Gap 11
Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1.backl 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Database:

Statistics: Mean 30.064; Variance 126.027; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

22 22	20	19	18	17	16	15	14	13	12	11	10	. 6	8	7	o	ъ	4	w	N	_	Result
183	183	210	212	221	221	225	225	284	318	324	337	589	666	912	979	994	994	1227	1306	1306	Score
αα 4.4	. 8	9.6	9.7	10.1	10.1	10.3	10.3	13.0	14.6	14.8	15.4	27.0	30.5	41.8	44.8	45.5	45.5	56.2	59.8	59.8	Query Match 1
595 595							325	39	43	40	41	153	158	157	124	167	167	199	455	455	Length [
5 ~	5	IJ	۲	0	u	5	u	7	7	7	7	7	7	7	7	7	7	7	7	7	BB
US-08-570- US-08-225-	PCT-US96-1	US-08-292-	5395760-4	PCT-US91-0	US-08-292-	PCT-US91-0	US-08-292-	US-08-050-	US-08-050-	us-08-050-	us-08-050-	us-08-050-	us-08-050-	US-08-050-	us-08-050-	us-08-050-	us-08-050-	us-08-050-	us-08-050-	US-08-321-	ID
Sequence 2, Sequence 2,	'n	Sequence 6,	Patent No. 5	Sequence 4,	٠,	Sequence 2, 1	Sequence 2, 1		Sequence 31,		Sequence 36,	Sequence 52,		50,	4	Sequence 57,	Sequence 2, i	Sequence 48,	Sequence 25,	Sequence 2, i	Description
Applicatio Applicatio	Applicatio	Applicatio	5395760.	Applicatio	Applicatio	Applicatio	Applicatio	Applicati	Applicati	Applicati	Applicati	Applicati	Applicati	Applicati	Applicatio	Applicati	Applicatio	Applicati	Applicati	Applicatio	1 1 1 1 1 1 1 4
1.06e-07 1.06e-07		3.86e-10	2.54e-10	3.81e-11		1.64e-11	1.64e-11		.09e-	8.28e-21	.74e-	1.12e-46					3.05e-87	8.08e-111	7.75e-119	7.75e-119	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	
155	155	160	160	160	165	169	169	169	169	167	167	167	167	180	180	180	180	181	181	181	181	1
7.1	7.1	7.3	7.3	7.3	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	8.2	8.2	8.2	8.2	8.3	8.3	8.3	8 . u	
438	206	217	198	177	186						93	71	70	518	486						228	
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US-08-097-	US-08-097-	US-08-187-	US-08-187-	US-08-187-	US-08-089-	PCT-US93-0	US-08-453-	PCT-US93-0	US-08-453-	US-08-343-	US-08-445-	US-08-314-	US-07-920-	US-08-385-	US-08-243-	5395760-2	US-08-385-	PCT-US95-0	PCT-US94-0	US-08-453-	US-08-188-	
Sequence			Sequence	Sequence		Sequence	Patent No	Sequence	Sequence	Sequence	Sequence	Sequence	1 1 1 1 1									
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٠	3.10e-05	1.14e-05	1.14e	1.14e	4.16e		. 85e	. 85e	1.85e-06	2.77e-06		2.77e-06	2.77e-06		1.96e-07		1.96e-07	1.59e-07			1.59e-07	

# ALIGNMENTS

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TELEX: 248633			TELECOMMONICATION INFORMATION:	BITTING TO THE CONTRACT OF THE	•	RATION NUMBER:	NAME: BROWDY, Roger L.		FILING DATE: 12-OCT-1993	2	1	PRIOR APPLICATION DATA:	CLASSIFICATION: 435	FILING DATE: 12-OCT-1994	APPLICATION NUMBER: US/08/321,668	CURRENT APPLICATION DATA:	SOFTWARE: Patentin Release #1.0, Version #1.30	OPERATING SYSTEM: PC-DOS/MS-DOS	COMPUTER: IBM PC compatible	м	ᄣ	ZIP: 20004	COUNTRY: USA	C	_	-:	E: BROWDY AND NEIMARK	CORRESPONDENCE ADDRESS:	NUMBER OF SEQUENCES: 42		INVENTION: MOLECULES INFLUENCING THE SHEDDING OF	APPLICANT: BATKIN, MICHAEL	VARFOLO	APPLICANT: BRAKEBUSCH, CORD	APPLICANT: WALLACH, David	GENERAL INFORMATION:	Patent No. 5665859	Sequence 2, Application US/08321668		Sequence 2, Application US/08321668.		01-JAN-1900 ·		XXXXX		US-08-321-668-2 STANDARD; PRT; 455 AA.	TLT 1

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   SEQUENCE
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                                                                    REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 25:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
MOLECULE TYPE: protein
JENCE 455 AA; 50579 MW; 1048388 CN;
                   SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 455 AA; 50494 MW; 1048031 CN;
                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Reed & Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: Californi
COUNTRY: USA
ZIP: 94301
                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 63
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 455 amino acids
                                                                                                                                                                                                                                                                                                 California
                                             455 amino acids
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                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE 199 AA; 22186 MW; 195553 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 48, Application US/08050319B
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                41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
                                                       Local Similarity
nes 156; Conser
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 23
                                                                                                                                                                                               TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 617-8999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 635 Bryant
CITY: Palo Alto
STATE: California
COUNTRY: USA
DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                     NAME: Robbins, Roberta I
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
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                                                    56.2%;
larity 98.1%;
Conservative
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                                                   Score 1227; DB 7;
Pred. No. 8.08e-111;
1; Mismatches 2;
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Pred. No. 7.75e-119;
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APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                           41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                               83
                                                                                                                                                           23
                                                                                                                                                                                                                                'Match 45.5%; Score 994; DB 7;
Local Similarity 99.2%; Pred. No. 3.05e-87,
Nes 126; Conservative 1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 167 AA; 18626 MW; 139513 CN;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                               SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
   KQNTVCT
                                         KQNTVCT 167
                                                                           SCSKCRREMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142
                                                                                                                                                   DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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   US-08-050-319B-4
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GENERAL INFORMATION:
                                                                                                                                                         143 KQNTVCT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 45.5%;
Local Similarity 99.2%;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-LOSS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
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APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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LENGTH: 167 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Robbins, Roberta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 amino acids
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   STANDARD;
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Pred. No. 3.05e-87;
Pred. No. 3.05e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57:
   PRT;
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RESULT RESULT OF THE COLOR OF T
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Best Local S
Matches 12
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NAME: ROBBITS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 627-3231
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEWIST. 1415-1615.
                                                                                                                                                            Sequence 50, Application US/08050319B
                                                                                                                                                                                                                                                                                                      US-08-050-319B-50
                                                                                                                                                                                                              01-JAN-1900
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Sequence 50, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08050319B Patent No. 5633145
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Local Similarity 99.2%;
nes 123; Conservative
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APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 10-May-1993
CLASSIFICATION: 435
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JENCE 124 AA; 14047 MW; 75840 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
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635 Bryant Street
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                                                                                                                                                                                                                                                                                                   STANDARD;
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Pred. No. 9.96e-86;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                      Sequence 54, Application US/08050319B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
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                                                                                                                                                                                                                                                                        Sequence 54, Application US/08050319B Patent No. 5633145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 QI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ENLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLP 179
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 ENLFOCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                       APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                              NUMBER OF SEQUENCES: 5
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NAME: Robbins, Roberta L.
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CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    STREET:
                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 41.8%;
1 Similarity 95.9%;
117; Conservative
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                                                Palo Alto
                      California
                                                                    635 Bryant Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 617-8999
(415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed & Robbins
                                                                                              Reed & Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 912; DB 7;
Pred. No. 5.63e-79;
2; Mismatches 3
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Query Match 30.5%;
Best Local Similarity 97.7%;
Matches 86; Conservative
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REGISTRATION NUMBER: 33,208
REFERENCE_DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RODDINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52, Application US/08050319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 SCSKCRKEMGQVEISSCTVDRDTVCTCH 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 SCSKCRKEMGQVEISSCTVDRDTVCGCR 110
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                          APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 10-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                      STREET: 635 Bryant
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LE TYPE: protein
158 AA; 17375 MW; 124033 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             READABLE FORM:
                                                                                                                                                                                                                                 635 Bryant Street
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                                                                                                                                                                                                                                                 Reed & Robbins
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Pred. No. 2.50e-54;
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                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBbins, Roberta L.
REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-050-319B-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.0%;
Local Similarity 69.8%;
les 81; Conserva+*...
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INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
                                                                           TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 CESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 CPQGKYIHPQNN-SIC--CTKCHK--GTYLYNDCPGPGQDT-DCRKNQYRHYWSENLFQC
                                                                                                                        REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein JENCE 153 AA; 17148 MW; 116104 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Modified human TNFalpha (Tumor TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: M.Feldmann, P.I
APPLICANT: M.J.C. Turner,
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                                                                                                                                                                                                                                                                                                                                                                    STATE: C
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TYPE: amino acid
                    TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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STREET: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
                                                                                                                                                                                                                                                                                                                                                         ZIP: 94301
                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                   Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                   California
                                                              41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                     USA
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M.J.C. Turner, F.M Brennan
                                  single
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Pred. No. 1.12e-46;
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                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                         COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
     XXXXXX
                           US-08-050-319B-31
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                                                                       25 VCPQGKYIHPQNNSICCTXCHKGTYLYNDCPGPGQDTDCR 64
                                                                                                                     / Match 14.8%; Score 324; DB 7; In Local Similarity 100.0%; Pred. No. 8.28e-21; les 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Local Similarity 97.6%;
                                                                                               1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: C
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                                                                                                                                                                      LE TYPE: protein 40 AA; 4459 MW; 7536 CN;
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635 Bryant Street
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Pred. No. 4.74e-22;
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                           PRT;
                                                                                                                                              DB 7; Length 40;
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Best Local S
Matches 4
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INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                Sequence 40, Application US/08050319B.
                                                                                                                                                         01-JAN-1900
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                                                                                              Sequence 40, Patent No. 56
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Patent No. 5
                                                                                                                                                                                                                                                                                                   y Match 14.6%;
Local Similarity 100.0%;
hes 43; Conservative
                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     1 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 617-8999
        APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Mecrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
BADDICCATTON MIMEER: 18/08/080 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human INFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0
FILING DATE: 10-May-1993
CLASSIFICATION: 435
 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                    LE TYPE: protein
43 AA; 4767 MW; 9758 CN;
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Reed & Robbins
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Pred. No. 3.09e-20;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 97.4%;
les 38; Conservation
                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                 COUNTRY: USA
ZIF: 98101
ZIF: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/292,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33.208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415), 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 10-May CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
                            CLASSIFICATION: 530
                                                                                                                                                                                 STREET: 51 Uni
CITY: Seattle
                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE TYPE: protein
39 AA; 4335 MW; 8059 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94301
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                                                                                                                                                                    Washington
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51 University Street
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  07/963,330
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Pred. No. 5.18e-17;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9102207 GENERAL INFORMATION:
                                 TELEFAX: (206) 587-060
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 34.8%; nes 39; Conservation
                                                                                   APPLICATION NUMBER: PCT/US91/
FILING DATE: 19910329
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2602
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F0RMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 587-04
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LLAFGLICLPWIQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC
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                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
NODITATION NUMBER: PCT/US91/022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists
NUMBER OF SEQUENCES: 4
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ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,69
                                                                                                                                                                                                                                                                                             COUNTRY:
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325 AA; 35132 MW; 591446 CN;
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                      H: 325 amino acids
AMINO ACID
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51 University Street
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              linear
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Pred. No. 1.64e-11;
21; Mismatches 45
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed May 6 10:56:07 1998; MasPar time 65.66 Seconds 920.693 Million cell updates/sec

Description: Perfect Score: N.A. Sequence: >US-08-804-166-5 (1-1147) from US08804166.seq 1147 1 TCGAGATGGCTACAGGTAAG......
AGCTCTACCGATGTCCATTC.....

.AATCTTAAGGATCCCTCGAG 1147

Scoring table: Gap TABLE default Gap 6

Nmatch

Searched: 102136 seqs, 26354296 bases x 2

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-1ssued 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 8.727; Variance 4.288; scale 2.035

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Length DB	BB	ID	Description	8		Pred. No.
1	506	44.1	2062	7	US-08-050-	Sequence	2	, Applicati	0.00e+00
N	506	44.1	2175	7	US-08-321-	Sequence	Ļ	Applicatio	0.00e+00
ω	504	43.9	6889	14	PCT-US95-0	Sequence	ρ	Applicatio	0.00e+00
4	504	43.9	6889	σ	US-08-286-	Sequence	Ņ	Applicatio	
ر ت	464	40.5	600	7	US-08-050-	Sequence	47		0.00e+00
თ	375	32.7	504	7	US-08-050-	Sequence	56	Applicati	
7	373	32.5	501	7	US-08-050-	Sequence	1,	Applicatio	4.58e-291
8	364	31.7	372	7	US-08-050-	Sequence	ω,	Applicatio	2.74e-283
9	345	30.1	474	7	US-08-050-	Sequence	49,	Applicati	6.94e-267
10	288	25.1	2771	7	US-08-273-	Sequence	5	Applicatio	8.12e-2
11	287	25.0	4283	7	US-08-343-	Sequence	ω	Applicatio	5.86e-
12	287	25.0	4283	7	US-08-445-	Sequence	۳	Applicatio	5.86e-2
13	255	22.2	477	7	US-08-050-	Sequence	53	, Applicati	1.56e-189
14	213	18.6	462	7	us-08-050-	Sequence	51	, Applicati	1.02e-153
15	67	5.8	534	σ	US-08-187-	Sequence	ω	Applicatio	4.70e-33
16	67	5.8	654	σ	US-08-187-	Sequence	,1	Applicatio	4.70e-
17	58	5.1	321	σ	US-08-314-	Sequence	23	, Applicati	3.86e-2
18	58	5.1	321	4	US-07-920-	Sequence	23	, Applicati	3.86e-2
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quence 24, per tent No. 563 ENERAL INFOHAPPLICANT: TITLE OF IN NUMBER OF SCORRESPONDE STREET: CITY: PASTATE: COMPUTER REDIUM TY COMPUTER REPERANCE CURRENT APPLICANT PAPLICANT PELLENGARE REGISTRATE: COMPUTER RETERENCE CURRENT APPLICANT PELLENGARE REFERENCE REGISTRATE: REFERENCE REGISTRATE: REFERENCE TELLECOMMUNIA TELLEPANS REFERENCE TELLEPANS REFERENCE TELLEPANS REFERENCE REGISTRATION FILLOMMUNIA TELLEPANS REFERENCE REGISTRATION FILLOMMUNIA REFERENCE REGISTRATION FILL	nce 24	'AN-1900	×	1 -050-31		2255	2 2 2 2 5 5 6 8	5 5 5 5 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6
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quence 24, Application US/0805 tental INFORMATION: APPLICANT: M.Feldmann, P.W. APPLICANT: M.Feldmann, P.W. APPLICANT: M.J.C. Turner, F. TITLE OF INVENTION: Modified TITLE OF INVENTION: Modified TITLE OF INVENTION: Mccrosis NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS: STREET: 635 BIYANT Street CITY: Palo Alto STREET: California COUNTRY: USA COUNTRY: USA COUNTRY: USA COMPUTER: IBM PC COMPATION SOFTWARE: PAPPLICATION DATA: MEDIUM TYPE: Floppy disk COMPUTER: IDM PC COMPATION SOFTWARE: PAPPLICATION DATA: APPLICATION NUMBER: US/08/FILING DATE: 10-May-1993 CLASSIFICATION: 435 ATTORNEY/ACENT INFORMATION: NAME: RODDINS, RODERTA L. REGISTRATION NUMBER: 33,20 REFERENCE/DOCKET NUMBER: 5 TELEPHONE: (415) 617-8999 TELEPAX: (415) 617-8999 TELEPAX: (415) 617-3231 NFORMATION FOR SEQ ID NO: 24:	US			RD; DNA	ALIC			7 US-08
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                                                                                                      Sequence 1, Patent No.
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NAME/KEY: CDS

LOCATION: 155..1519

Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;
                                                                                                                                    Sequence 1,
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                                                                                                                                                                                                          US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP
                                                                                                                                                                                                                                                                                                                                                                            644
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APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING
TITLE OF INVENTION: THE THF RECEPTORS, THEIR PREPARATIC
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA to
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                                                                                                                                                                                                                                                  AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                   h 44.1%;
Similarity 98.1%;
                                                                                            INFORMATION:
                                                                                                       , Application US/08321668 5665859
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Pred. No. 0.00e+00;
0; Mismatches 9
                               THEIR PREPARATION AND
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Best Local Similarity 98.1%;
Matches 521; Conservative
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION OATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 256..1620
Sequence 2175 BP; 474 A;
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                              AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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             TCCTGTAGTAACAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
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TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG
                                                                                                 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG
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Best Local S
Matches 50
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                    464
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                                                                                          344 GATAGTGTGTCCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        824
                                                                                                                            Local Similarity 99.0%;
les 509; Conservation
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
TITLE OF INVENTION: HOST CELLS
                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/2: FILING DATE: 05-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                      AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC
AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                 TGCAGGGAGTGTGAGAGCGGCTTCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                    TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
                                                                       AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
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460 Point San Bruno
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Pred. No. 0.00e+00;
0; Mismatches 5;
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APPLICANT: Crowley,
TITLE OF INVENTION:
TITLE OF INVENTION:
                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6889 bases
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                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 05-AU
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ZIP: 94080
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STRANDEDNESS:
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double
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METHOD FOR
HOST CELLS
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Sequence 6889 BP; 1729 A;
                                                                                                                                                                                           Sequence 47, Application Patent No. 5633145
                                                                                                                                                                                                                                                                                                        US-08-050-319B-47 STANDARD;
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                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                        APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS
                                                      CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                          TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
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                                             ZIP: 94301
                                                                                                  ADDRESSEE:
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Similarity 99.0%;
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                                                                                       E: Reed & Robbins
635 Bryant Street
PC-DOS/MS-DOS
                                                                                                                                                                                                     US/08050319B
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                                                                                                                                                                                                                                                                                                        DNA; UNC; 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 504; DB 6; Pred. No. 0.00e+00;
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Best Local Similarity 98.3%;
Matches 472; Conservative
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                                                                                                                                                           764
                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Robbins, Roberta L.
REFERENCE/DOCKET NUMBER: 33.208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION
                                                                                                                                                                   TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCCTACCCCCAGATTTAG
                                                                                                                                                                                                    CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAAGTGAAAACCTT
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                                                                                                                                                         TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 1..597
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                                                                                                             STANDARD;
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                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 464; DB 7;
Pred. No. 0.00e+00;
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                                                                                                            UNC; 504
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Sequence 56, Application US/08050319B Patent No. 5633145 Sequence 56, Application US/08050319B

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Query Match
Best Local S
Matches 37
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NAME: ROBDINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1..501
Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: M.Feldmanu, APPLICANT: M.J.C. Turner, F.M. Brennan APPLICANT: M.J.C. Turner, F.M. Brennan TNFalpha (Tumor TITLE OF INVENTION: Mccrosis Factor alpha) Receptor TITLE OF INVENTION: ACTORISE FACTOR ALPHA) Receptor TITLE OF ENGLISHED ST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-MAy-1993
CIASTIFICATION. A25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA to mRNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Reed & F
STREET: 635 Bryant
CITY: Palo Alto
STATE: California
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COUNTRY: US
ZIP: 94301
                                                                                                                     GATAGTGTGTGCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403
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TOPOLOGY: 11
AAACAGAACACCGTGTGCACCTG 503
                                                              TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                                  CGGGACACCGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                              AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                    TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                   AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC
                                          TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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Pred. No. 8.54e-293;
0; Mismatches 4;
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Best Local S
Matches 37
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NAME: ROBbins, Roberta L.
REGISTRATION NUMBER: 3,208
REFERENCE/DOCKET NUMBER: 5150-0030
REFERENCE/DOCKET NUMBER: 5150-0030
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEPRAY: (415) 617-831
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..501
Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08050319B Patent No. 5633145
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                       301
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                                                                                                                                             121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
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                                                                                                                                                                                            y Match 32.5%; Score 373; DB 7; Length 501: Local Similarity 99.0%; Pred. No. 4.58e-291; hes 377; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                              AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCCAGGATACCGAC
                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435
                                                                                                                   AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                            501 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 Bryant Street
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                                                                                                                                                                                                                   Length 501;
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                                      Query Match
Best Local :
                                                                                                                TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                       APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 31,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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1 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Recepton
NUMBER OF SEQUENCES: 57
                                                                                           FEATURE:
                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                   MOLECULE TYPE:
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                                                         NAME/KEY: CDS
LOCATION: 1.372
ence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                             TOPOLOGY:
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                             h 31.7%;
Similarity 98.9%;
368; Conservative
                                                                                                                                                                                                                                                                                                              94301
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635 Bryant Street
                                                                                                            linear
                                                                                                  DNA (genomic)
                                     Score 364; DB 7; Length 372; Pred. No. 2.74e-283;
                             Mismatches
                             Indels
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ID US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49, Application US/08050319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1900
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTTCCAG
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                                                        TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTGTTGCACAGTGGACCGGGAC
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                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ROBbins, Roberta L.
REGISTRATION UNBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAGAAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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  LENGTH:
474 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 Bryant Street
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                                                          49:
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Patent No. 5625124
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-273-411-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..471
Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08273411.
                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1900
                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 AGAGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 30.1%;
Local Similarity 98.3%;
hes 351; Conservative
                                                                                                                                                                                                                                              APPLICANT: Falk, Per APPLICANT: Gordon, Jeffrey I. TITLE OF INVENTION: Disease TITLE OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA to FEATURE:
                                                                                                                COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCCTGCCAGGAGAAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACACCGTGTGTGGCGGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGG 237
                                                                                                                                                                              CITY: Atlanta
STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCC
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                                                                                                                                                                                                      1100 Peachtree Street,
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                                                                                                                                                                                                                    Patrea L. Pabst
                                                                US/08/273,411
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Pred. No. 6.94e-267
0; Mismatches 6
                                                                                                                                                                                                        Suite 2800
                                                                                                                                                                                                                                                                   for Gastro-Intestinal
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ID US-08-343-401A-3
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Best Local S
Matches 32
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TELEPHONE: (404) 815-6508
TELEPAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                  306
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AUTHORS: Sweetser, et al.
JOURNAL: J. Biol. Chem.
VOLUME: 261
PAGES: 5553-5561
DATE: 1986
                                                                                                                                                                               66
                                                                                                                                                                                                                                                                                                                                                                                                                   RELEVANT RESIDUES IN SEQ
PUBLICATION INFORMATION:
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                                 GCCTGCTCTGCCTGCCTGGCTTCAAGAGGGCAGTGCC 1013
                                                                                                                   GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC
                                                                                                                                         AUTHORS:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
JOURNAL:
VOLUME:
                                                                                                        GGAGAGAAAAAACAAACAGCTCCTGGAGCAGGGACACTCCTGGCCTCTTGCTCTGCGGC
                                                                                      TCCCTCTGTTGCCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG
                                                                                                                                                                                                                                                                                                                                                                         PAGES: 239-249
DATE: 1982
                                                                     TCCGTGTGTTGCCCTGTGGTTTCTCCCCACGCTCCCGGACGTCCCTGCTCCTGGCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGES: 1310
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                     ch 25.1%;
l Similarity 95.6%;
323; Conservative
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STANDARD;
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DNA;
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UNC;
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01-JAN-1900

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Sequence

Application US/08343401A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:

NAME: Seay, NICHOLAS J

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 11-2:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEPAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 4283 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: sig_peptide
LOCATION: 713..1049
Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/343,401A
FILING DATE: 22-NOV-1994
CLASSIFICATION: 514
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Patent No. 5661132
                                                      832
                                                                                                                                                            772
                                                                                                                                                                                                                                    713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
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APPLICANT: Andree, Christophe
TITLE OF INVENTION: Improved Wound Healing
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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CLONE: pWRG1630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
                                                                                                                                                                                                        HITTHE AND A TOGCTACAGGTAAGCGCCCCTAAAATCCCTTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65
                                              TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
                                                                                                CAGCGACCTGTAGATGGGACGGGGCACTAACCCTCAGGTTTGGGGGCTTTTGAATGTGAG 125
TATGGCCATGTAAGCCCAGTATTTGCCCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
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Macklin, Michael D
Eriksson, Elof
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981..1253
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713..721
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                       Query Match
Best Local S
Matches 31
                                                                   NAME/KEY: CDS
LOCATION: join(713..721, 981..1250)
Sequence 4283 BP; 1023 A; 1095 C; 1114 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08445265A Patent No. 5697901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08445265A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JENERAL INFORMATION:
APPLICANT: ETIKSSON, E1
TITLE OF INVENTION: GEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                      Match 25.0%;
Local Similarity 93.2%;
les 315; Conservative
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,265A
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            CLASSIFICATION: 604
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 273
                                                                                                        FEATURE:
                                                                                                               MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Plasmid DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGAGAGAAAAACAAACAAACACTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCCCGGC
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                                                                                                                                                     TYPE: nucleion STRANDEDNESS:
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                                                                                                                                          TOPOLOGY: circular
                                                                                                                                                                            LENGTH:
                                                                                                                                                               nucleic acid
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                                                                                                                                                                           4283 base pairs
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                   Score 287; DB 7; Len, Pred. No. 5.86e-217;
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                                                                     1051 T; 0 other;
                                             Length 4283;
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                      Gaps
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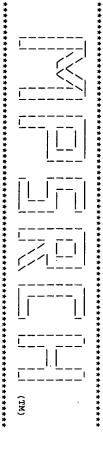
ATGCTTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGAGG 65

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                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
NAME/KEY: CDS
LOCATION: 1..474
Sequence 477 BP; 117 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
TITLE OF SECUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-050-319B-53 STANDARD; DNA; UNC; 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 53, Application US/08050319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1900
                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBDINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 53, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306
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                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                      MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
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                                                                                                                                                                                                                                                                                                                                                                                   STREET: 635 Bryan
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
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                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                            STRANDEDNESS:
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                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                              635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                 linear
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                                                    cDNA to mRNA
                                                                               double
122 C; 131 G; 107 T;
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0 other;
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Best Local Similarity 98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                        NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-050-319B-51 STANDARD; DNA; UNC; 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51,
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                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                           ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                            STREET: OJ.
STREET: Palo Alto
CITY: Palo Alto
CTATE: California
                                                                                                                                                                                                                                                                                                                                 APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, version CURRENT APPLICATION DATA:
                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGACACCGTGTGTACCTGC 381
         LENGTH: 462 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 10-May-1993
                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258;
                                                                                                                                                                                                                                                                                                                                                                                                     l, Application US/08050319B 5633145
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Pred. No. 1.56e-189
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                                                                                                    5150-0030
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ID US-08-187-756C-3 STANDARD; DNA; UNC; 534 BP.
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Best Local Similarity 97.8%;
Matches 218; Conservative
        NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE_DOCKET NUMBER: 325800-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1..459
Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                    Patent No. 5597709
GENERAL INFORMATION:
APPLICANT: ROSEN,
                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08187756C Patent No. 5597709
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08187756C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 660
                                                                                                                 APPLICATION NUMBER: US/08/187,756C FILING DATE: January 27, 1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                       COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                     APPLICANT: ROSEN, ET AL.
TITLE OF INVENTION: Human Growth Hormone
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                     ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                       COUNTRY:
534 BASE PAIRS
                                                                                                                                                                                                                                                      USA
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Pred. No. 1.02e-153
0; Mismatches 5
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Search completed: Wed May Job time: 87 secs.
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                                                                                                                                      Matches
                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
Sequence 534 BP; 108 A; 166 C; 143 G; 117 T; 0 other;
                                                                                        333 AGGGCAGTGCC
                                                          68 AGGGCAGTGCC
                                                                                                                                   Match 5.8%;
Local Similarity 97.2%;
es 69; Conservative
                                                                                                              8 CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGGCTTCAAG
                                                                 78
                                             343
           6 10:57:34 1998
                                                                                                                                   Score 67; DB 6; L
Pred. No. 4.70e-33;
0; Mismatches 2
                                                                                                                                                         Length 534
                                                                                                                                      Indels
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                                                                                                                                     Gaps
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed May 6 08:20:59 1998; MasPar time 4.78 Seconds 367.559 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-804-166-4 (1-307) from US08804166.pep 2341

Scoring table: PAM 150 Gap 11 1 SRTSLLLAFGLLCLPWLQEG......PSLPSPSRLPGPSDTPILPQ 307

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 30.606; Variance 140.802; scale 0.217

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description	Pred. No.
ב	1124		455	7	US-08-321-	Sequence 2, Applicatio	4.13e-91
N	1124	48.0	455	7	-80-	25, App	4.13e-91
ω	1115	•	199	7	us-08-050-	48,	.79e-9
4	1025	43.8	145	σ	-8	2, A	5e-8
ر.	1025	•	145	σ	-8	1, Appl	.45e-8
6	1020	•	145	7	US-08-298-	,1	.57e-8
7	995	•	145	σ	-80	e 10	3.13e-7
- σο	996	•	167	7	90-	57	2.54e-7
9	996		167	7	US-08-050-	2	2.54e-7
10	981		124	7	US-08-050-	Sequence 4, Applicatio	6.07e-7
11	800	•	157	7	US-08-050-	50	2.36e-6
12	740	•	114	σ	-80-	9	7.01e-5
13	734		114	σ	US-08-425-	7,	2.47e-5
14	714	•	117	o	-80-	11	1.63e-5
15	684	•	114	σ	8	8	8.72e-5
16	666	•	158	7	-8	54	3.76e-4
17	651		117	σ	US-08-425-	12	8.62e-4
18	613		149	σ	-8	Sequence 5, Applicatio	2.38e-
19	477		153	7	us-08-050-	Sequence 52, Applicati	4.02e-3
20	339		41	7		36	6.36e-
21	324		40	7		26	1.29e-
22	318	13.6	43	7	US-08-050-	Sequence 31, Applicati	4.28e-

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Seque GENEE GENEE GENEE APP APP APP CO CO CO CO TE TI	Sequenc	01-ர	xxxxx	US-08	;	22222222222222222222222222222222222222
quence 2, a tent No. 56 ENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CORRESPONI ADDRESSE STREET: COUNTRY: STATE: COUNTRY: COMPUTER F COMPUTER F COMPUTER F PRIOR APPLICAT FILING I CLASSIET APPLICAT FILING I FILING I FILING I FILING I FILING I APPLICAT FILING I APPLICAT FILING I FILING I APPLICAT FILING I APPLICAT FILING I APPLICAT FILING I FILING I APPLICAT FILING I APPLICAT APPLICAT FILING I APPLICAT FILING I APPLICAT APPLICAT FILING I APPLICAT APPLICAT FILING I APPLICAT APPLICAT APPLICAT FILING I APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLICAT APPLI	Ø	JAN-1900	×	1 8-321-	;	200101010101010101010101010101010101010
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ion US/08:  CH, David BUSCH, Co LOMEEV, En N, Michael N	JS.			STANDARD;	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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EPARATION						5451527.  Applicatio Applicatio Applicati Applicati Sympolicati Sympolicati Applicati Applicati Applicati Applicati Applicati Applicati Applicati Applicati Applicati Sympolicati Applicati
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                     ATTORNEY/AGENT INFORMATION:

NAME: ROBOTIS, ROBETTE L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

RELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEPEAX: (415) 27-3231

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: mino acids
  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08050319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 KONTVCTCHAGFFLRENECVSCS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQQDTDCRECESGSFTASENHLRHCL 100
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                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
 MOLECULE TYPE: protein
JENCE 455 AA; 50579 MW; 1048388 CN;
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 455 AA; 50494 MW; 1048031 CN;
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
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STATE: Californ
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Similarity 99.3%;
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Pred. No. 4.13e-91;
1; Mismatches 0
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Best Local :
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                                                                                                       SEQUENCE
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 5150
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-050-319B-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48, Application US/08050319B
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APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 KONTYCTCHAGFFLRENECVSCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 KQNTVCTCHAGFFLRENECVSCS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
                        41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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                                                                                                  LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
QUENCE 199 AA; 22186 MW; 195
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: COLLING CITY: Palo Alto CITY: California
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
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Similarity 99.3%;
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larity 98.6%;
Conservative
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                                                 Score 1115; DB 7;
Pred. No. 2.79e-90;
1; Mismatches 1
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Pred. No. 4
                                                                                                    195553 CN;
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No. 4.13e-91;
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                                                                                        Match 43.8%;
Local Similarity 99.3%;
             67
                                TELEFAX: (609) 466-276
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,673
FILING DATE:
CLASSIFICATION: 514
DETGE ADDITION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
TITLE OF INVENTION: Methods For Preparing and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-JUN-1991
                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (609) 466-3407
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IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSSKAPPP 126
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                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                              138;
                                                                                                                                                                     LENGTH: 145 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                 NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD 1.0-004
                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                           145 AA; 15544 MW; 114662 CN;
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                                                                                        Score 1025; DB 6;
Pred. No. 5.45e-82;
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                                                                              0; Mismatches
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                                                                                                                                  SEQUENCE
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  229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP
                     67
                                                                                      Local Similarity
les 138; Conser
                                                                                                                                                                                                         TELEFAX: (609) 466-2760 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                 7
                                                                                                                             HYPOTHETICAL: NO
ANTI-SENSE: NO
JENCE 145 AA; 15544 MW; 114662 CN;
                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: UNTELECOMMUNICATION INFORMATION: TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ME NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moyle, APPLICANT: Campbe
                                          PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
                                                       PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
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 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP
          IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
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CITY: PI
STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                          NAME: Muccino, Richard R. REGISTRATION NUMBER: 32,538
                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 0855
                                                                                                                                                                                                 LENGTH:
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                                                                                     43.8%;
llarity 99.3%;
Conservative
                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Jersey
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Box 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Analogs of Glycoprotein Hormones Having
Altered Receptor Binding Specificity and
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                                                                                     Score 1025; DB 6;
Pred. No. 5.45e-82;
0; Mismatches 1
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                                                                                                           Length 145;
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ID US-08-298-189B-1
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                       Query Match
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Matches 13
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NAME: Brian D. Voyce
REGISTRATION NUMBER: 28,917
REFERENCE/DOCKET NUMBER: DSI1
TELECOMMUNICATION INFORMATION:
TELEPAN: 919-638-3939 or 803-272-1471
TELEFAX: 919-638-3939 or 803-272-1471
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: NO. 5674727 applicable
TOPOLOGY: Unknown
                                                                     DATE:
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08298189B.
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GENERAL I
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7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
                                                                                                                                                     IDENTIFICATION METHOD: N-1
PUBLICATION INFORMATION:
AUTHORS: Keutmann et alia
                                                                                                                                                                                                                                      MOLECULE TYPE: subunit of hormone, specifically MOLECULE TYPE: beta\subunit of hCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOTTWARE, MACROSOFT WORD 7.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" di
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TITLE OF INVENTION:
                                                                                                                                                                                                                  ORIGINAL SOURCE: FEATURE:
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                                                                                                                   AUTHORS: Keutmann et ....
TITLE: "A Receptor-binding Region in
JOURNAL: Proc Nat'l Acad Sci USA
                                                                                                       ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US
FILING DATE: 08/31/94
CLASSIFICATION: 435
                                                                                            PAGES:
                                                                                                                                                                                           NAME/KEY: beta subunit of hCG that is nicked by GBNE LOCATION: hCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                       l Similarity
137; Conser
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                                                                      145 AA; 15476 MW; 116769 CN;
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                      43.68;
llarity 98.68;
Conservative
                                                                                             No. 5674727 applicable 2038-2042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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VENTION: No. 5674727el Methods for Detectin
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                                                                                                                                                                                                                              human urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laurence A. Cole , c/o Dept. of Obstetrics and
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                      Score 1020; DB 7; I
Pred. No. 1.57e-81;
2; Mismatches 0;
                                                                                                                                                                            N-terminal sequence analysis
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                                                                                                                                           Human
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                                             Length 145;
                       Indels
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Matches 13
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HYPOTHETICAL: N
ANTI-SENSE: NO
SEQUENCE 145 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                Local Similarity
nes 134; Conser
                                                                                                                                                 TELEFAX: (609) 466-2760 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 145 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and
TITLE OF INVENTION: Methods For Preparing and Using Same
                                                                                                                                                                                                                                FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R
REGISTRATION NUMBER: 32,
                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,673
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLFALPQVVCNYRDVRFES
                                                                                                                          SLPSPSRLPGPSDTPILPQ 307
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                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US (FILING DATE: 18-JUN-199)
                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 0855
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Richard R. Muccino
STREET: P.O. Box 1267
                                                                                                                                                                                                                                                                                                                                                                                                                               Princeton 
: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0, Application US/08425673
5508261
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llarity 96.4%;
Conservative
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                                                                               15448 MW; 114931 CN,
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                                                                                                                                                                                                                                 32,538
                               Score 995; DB 6;
Pred. No. 3.13e-79;
1; Mismatches 4
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PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

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Query Match 42.5%;
Best Local Similarity 100.0%;
Matches 127; Conservative
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NAME: ROBBITS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEPAX: (415) 327-3331
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57, Application US/08050319B
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APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor
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                                                                                                     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94301
COMPUTER READABLE FORM:
                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 167 AA; 18626 MW; 139513 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
            KQNTVCT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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KQNTVCT 149
                                                                                         DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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                                             SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
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                                                                                                                                     Score 996; DB 7;
Pred. No. 2.54e-79;
0; Mismatches 0
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01-JAN-1900
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                                                                                                                                                                                                                                                                                 SEQUENCE
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US-08-050-319B-4
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                                                                                                 161 KQNTVCT 167
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                                                                                                                                                                                                                                 23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                                        41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein proce 167 AA; 18626 MW; 139513 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Palo Alto
CITY: Palo Alto
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: M.J.C. Turner, F.M Brennau
APPLICANT: M.J.C. Turner, F.M Brennau
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
TITLE OF STONENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                    KONTVCT 149
                                                                                                                                                                                           SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version
                                                                                                                                                                                                                                                                                                      127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/050,319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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  STANDARD;
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er, F.M Brennan
                                                                                                                                                                                                                                                                                                            Score 996; DB 7; Lo
Pred. No. 2.54e-79;
0; Mismatches 0;
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Query Match
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Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein SEQUENCE 124 AA; 14047 MW; 75840 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08050319B.
  Sequence 50, Application US/08050319B Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319B

FILING DATE: 10-May-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: PORNTISS POPERATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Applic Patent No. 5633145
                                                                                                                                                                                                                                                                                                                                                                           145 NTVC 148
                                                                                                                                                                                                                                                                                                                                                                                                                      121 NTVC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 41.9%;
Local Similarity 100.0%;
les 124; Conservative
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APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REGERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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       M.J.C. Turner, F.M Brennan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                           US/08050319B.
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Pred. No. 6.07e-78;
0; Mismatches 0
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Best Local 9
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REGISTRATION NUMBER: 33.208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 and no acids
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08425673.
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                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08425673 Patent No. 5508261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165
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TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYPE: No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119
                                                                                                                                                                              APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity
TITLE OF INVENTION: Methods For Preparing and Using Same
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                     STREET: P.O. Bo:
CITY: Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435
                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 34.2%;
Similarity 96.2%;
102; Conservative
                         0855
                                                                  New Jersey
                                                                                                P.O. Box 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 Bryant Street
                                               USA
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Pred. No. 2.36e-61;
                                                                                                                                      Muccino
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Best Local Similarity 93.3%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                              US-08-425-673-7
                                                                                                                                                                                                                                                             Sequence 7, Application US/08425673
                                                                                                                                                                                                                                                                                     01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC
                                                                                                                                                                                                                               Sequence 7, Application US/08425673 Patent No. 5508261
                                                                                                                                                                                                                                                                                                                                                                                67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDCGGPKDHDSYC 110
                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (609) 466-2760 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                            APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and
TITLE OF INVENTION: Methods For Preparing and Using Same
NUMBER OF SEQUENCES: 12
ZIP: 08551

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD 1.0-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                    COUNTRY:
                                                                                                STATE:
                                                                                                         STREET: P.O. Bo
CITY: Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Muccino, Richard R. REGISTRATION NUMBER: 32,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 AA; 12250 MW; 68564 CN;
                                                                                               New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 amino acids
                                                                                                                     P.O. Box 1267
                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 740; DB 6; Le
Pred. No. 7.01e-56;
1; Mismatches 6;
                                                                                                                               Muccino
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                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                             eptor Binding Specificity and Activity Preparing and Using Same
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                                                                                                                                                                                                                                                                                                                                                                       272
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RESULT SE OL XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08425673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCTVRGLGPSYCDDPR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUCCLINO, RICHARD R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                APPLICANT: Moyle, William R.
APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and
TITLE OF INVENTION: Methods For Preparing and Using Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                   APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 514
                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                STREET: P.O. BO
CITY: Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                         ZIP: 08551
                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 31.4%;
Similarity 91.7%;
99; Conservative
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                                                                                                                                                                                                  New Jersey
                                                                                                                                                                                                                                           Richard
                                                                                                                                                                                                                           Box 1267
                18-JUN-1991
                           US 07/717,151
                                                                                                                                                                                                                                           R. Muccino
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                                                                             US/08/425,673
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Pred. No. 2.47e-55;
0; Mismatches 9
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TELECOMMUNICATION INFORMATION: TELEPHONE: (609) 466-3407

REFERENCE/DOCKET NUMBER: NAME: Muccino, Richard R. REGISTRATION NUMBER: 32,5

32,538

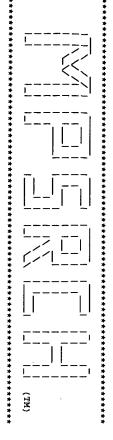
UMD 1.0-004

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-425-673-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08425673 Patent No. 5508261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/717,151
FILING DATE: 18 JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD 1.0-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.5%;
Local Similarity 98.9%;
98 93; Conservation
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,673
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                               APPLICANT: Moyle, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
TITLE OF INVENTION: Methods For Preparing and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Box 1
CITY: Princeton
STATE: New Jersey
                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                  ZIP: 08551
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                                                                          E: Richard R. Muccino
P.O. Box 1267
                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Pred. No. 1.63e-53;
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                                                                                   Query Match
Best Local :
                                                                          Matches
                                                                                                              SEQUENCE
                                    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262
                                                                    29.2%;
Local Similarity 94.7%;
hes 89; Conservation
          67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDC 100
                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                  LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                              114 AA; 12242 MW; 69571 CN;
                                                                                                                        ð
                                                                                                                               : peptide
                                                                        Score 684; DB 6;
Pred. No. 8.72e-51;
1; Mismatches 4
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                                                                         .
                                                                                           Length 114;
                                                                         Indels
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rch completed: Wed May time: 13 secs. σ 08:21:12 1998



Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 10:28:56 1998; MasPar time 67.26 Seconds 941.976 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: (1-1202) from US08804166.seq >US-08-804-166-3

N.A. Sequence: Comp:

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 102136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-1ssued 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 8.771; Variance 4.649; scale 1.887

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

18 19	16 17	14 15	13	:1:	10	. 80	7	σ	ر ت	4	ω	2	_	Result No.
6 6 9 9	88 99	169	255	301	302 300	370	379	381	420	424	424	424	424	Score
5.7	7.3	14.1 8.6	25.0	25.0	25.1 25.0	30.8	31.5	31.7	34.9	35.3	35.3	35.3	35.3	% Query Match
534 654	138 7218	462 138	4283	4283	2771 474	372	501	504	600	6889	6889	2175	2062	Length
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US-08-187- US-08-187-	US-08-086- US-08-232-	US-08-050-	US-08-445-	US-08-343-	US-08-273- US-08-050-	US-08-050-	US-08-050-	US-08-050-	US-08-050-	PCT-US95-0	US-08-286-	US-08-321-	US-08-050-	Ħ
Sequence 3 Sequence 1	Sequence 1	Sequence 5: Sequence 2,	Sequence 1. Sequence 5:		Sequence 5,	Sequence 3,	Sequence 1,	Sequence 50	Sequence 47		Sequence 2,	Sequence 1,	Sequence 24	Description
Applicatio Applicatio	Applicatio Applicati	l, Applicati , Applicatio	, Applicatio 3, Applicati		•	, Applicatio	, Applicatio	5, Applicati	7, Āpplicati	, Applicatio	, Applicatio	, Applicatio	1, Applicati	<b>J</b>
8.57e-32 8.57e-32	5.92e-54 9.89e-46	1.03e-107 5.77e-57	5.54e-212 2.07e-175	5.54e-212	8.84e-213 3.47e-211	3.96e-267	2.43e-274	6.06e-276	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	Pred. No.

TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

8888888888888888888888888888888	X D	X Z	XAX	RES	o o
Sequence Patent   GENERAL APPL TITLL TITLL TITLL OURS CORR COMP ST COMP COMP COMP COMP RET RET TELB	Sequenc	01-JA	xxxxx	80-SD TTD	44444333333332222222222222222222222222
uence 24 ent no. 19 APPLICANI APPLICANI APPLICANI APPLICANI TITLE OF TORRESPOIL ADDRESS TORREST APPLICA A	nce 24,	JAN-1900	×	1 -050-	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
iequence 24, Application US/0805031 atent No. 5633145 GENERAL INFORMATION: APPLICANT: M.Feldmann, P.W. Gra APPLICANT: M.Feldmann, P.W. Gra APPLICANT: M.Feldmann, P.W. Gra APPLICANT: M.Feldmann, P.W. Gra APPLICANT: M.J.C. Turner, F.M. B TITLE OF INVENTION: Modified hu TITLE HU TITLE HU TITLE OF INVENTION: Modified hu TITLE HU TITLE HU TITLE OF INVENTION: Modified hu TITLE HU TITLE HU TITLE OF INVENTION: Modified hu TITLE HU TITLE HU TITLE OF INVENTION: Modified hu TITLE HU TITLE HU TITLE OF INVENTION: Modified hu TITLE HU TIT	, Applic			319B-24	**************************************
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us/0805  n, P.W. 1  rner, F.  modified Modified Necrosis 57 57 Street  which street  which street  us/08/M Release ara: us/08/ PC-DOS/M Release ara: us/08/ FRION:	US,			RD; DNA;	4 PCT 1 US - 1 U
	/08050319в			v; UNC;	US-07-920- US-08-187- US-08-76-76-76-76-76-76-76-76-76-76-76-76-76-
alpha) rersion	•			2062 BP.	Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 3 Sequence 4 Sequence 5 Sequence 6 Sequence 6 Sequence 6 Sequence 7 Sequence 7 Sequence 8 Sequence 8 Sequence 8 Sequence 9
Receptor					72244
o H					Applicati Applicatio
					1.20e-24 1.20e-24 1.20e-24 1.20e-24 1.20e-20 9.36e-20 9.36e-20 9.36e-20 9.36e-10 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09 4.31e-09

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                                                                                                            Sequence 1,
Patent No.
GENERAL IN
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LOCATION: 155..1519
Sequence 2062 BP; 429 A; 617 C;
                                                                                                                                                                                                         US-08-321-668-1 STANDARD; DNA;
                                                                                                                                              Sequence 1, Application US/08321668
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                                      APPLICANT: WALLACH, David
APPLICANT: WAREBUSCH, COID
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE THE RECEPTORS, THEIR PREPARATION AND THEIR
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                             CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                                                                                                                                                          AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                       ADDRESSEE:
STREET: 4
                                                                                                                                                                                                                                            TCCTGT
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                                                                                                                                                                                                                                                                            CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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l Similarity 99.8%;
425; Conservative
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                                                                                                           INFORMATION:
              Washington
                                                                                                                     Application US/08321668 5665859
        D.C.
                       E: BROWDY AND NEIMARK 419 Seventh Street, N
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Pred. No. 0.00e+00;
0; Mismatches 1
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                        N.W.,
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                        Suite
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Best Local Similarity 99.8%;
Matches 425; Conservative
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TELEX: 248633
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 256..1620
Sequence 2175 BP; 474 A;
705
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                                                                                                                   676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCAATGGGACCGTGCACCTCTCCTGCCAGGAG
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                                                                 736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTAAGAGAAAACGAGTGTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-638-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: IL 107268
FILING DATE: 12-CCT-1993
ATTORNEY_AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                   TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                       CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                           AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25,618
                         801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 C; 604 G; 456 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 424; DB 7;
Pred. No. 0.00e+00;
0; Mismatches 1
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US-08-286-740-2 STANDARD;

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Best Local S
Matches 42
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 6889 bases
                                                                                                        1845
                                                                                                                                                   1785
                     1965
                                                               1905
                                                                                                                                                                      TOPOLOGY: linear
Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;
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                                                                                                                              405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
SIREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
585
                                                                                     465
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                                                                                                                                                                                                                Match 35.3%;
Local Similarity 99.8%;
les 425; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0:
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                        AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
                                                                                                                           CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
                                                                                              TGCAGGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: REFERENCE/DOCKET NUMBER:
                                                                                   TGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crowley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craig W. METHOD FOR SELECTING HIGH-EXPRESSING HOST CELLS
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Pred. No. 0.00e+00;
0; Mismatches 1;
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                                                                             Query Match
Best Local 9
                                                                  Matches
                                                                                                                                                      APPLICATION NUMBER: 08/286740
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 798P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-1994
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEY SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 6889 bases
                                  1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
                                                                                                            LENGTH: 6889 bases
TYPE: nucleic acid
STRANDEDNESS; double
TOPOLOGY: linear
Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2145
1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9509576
GENERAL INFORMATION:
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                       345
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                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genertech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
TITLE OF INVENTION: HOST CELLS
                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTGT 770
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                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                ch 35.3%;
l Similarity 99.8%;
425; Conservative
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                                                                Score 424; DB 14;
Pred. No. 0.00e+00;
0; Mismatches 1
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                                                                                        DB 14; Length 6889;
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                                                                                                                                                                                                                                                                                     Sequence 47, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Recepton
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                     TELEFAX: (415) 327-323
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                 APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: ROBBINS, ROBERTA L. REGISTRATION NUMBER: 33,208 REFERENCE/DOCKET NUMBER: 5150-0030 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    765
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            SOFTWARE: Patentin Release #1.0, version #1.25
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
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STATE: California
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             600 base pairs
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                                                                                                                                                                                                                                                                  US-08-050-319B-56 STANDARD; DNA; UNC;
                                                                                                                                                                                             Sequence 56, Application US/08050319B
                                                                                                                                                                                                                  01-JAN-1900
                                                                                                            GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: Reed & RO
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                              COUNTRY: U
                                                  CITY: Palo Alto
STATE: California
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635 Bryant Street

Reed & Robbins

Receptor

USA

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LOCATION: 1..597
Sequence 600 BP; 148 A; 157
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                                                                                                               421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCAATGGGACCGTGCACCTCTCCTGCCAGGAG
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541 TCCTGT 546
                                465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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Local Similarity 99.3%;
les 423; Conservative
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FEATURE: CDS
NAME/KEY: CDS
LOCATION: 1..5
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                                               CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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Pred. No. 0.00e+00;
0; Mismatches 3
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Best Local
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REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAK: (415) 327-3331
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 1..501
Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;
Sequence 1, Application US/08050319B Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray, APPLICANT: M.J.C. Turner, F.M Bro
                                                                                                                                                              US-08-050-319B-1
                                                                        Sequence 1, Application US/08050319B
                                                                                                 01-JAN-1900
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Local Similarity 99.7%;
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FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RODDINS, RODEITA L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                            AAACAGAACACCGTGTGCACCTG 503
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TOPOLOGY: 11r
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                                                                                                                                                           STANDARD;
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                                                                                                                                                           DNA;
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Pred. No. 6.06e-276;
0; Mismatches 1;
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Best Local
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TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..501
Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                              121 GATAGTGTGTGCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTTGCTGTACC 180
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                         481 AAACAGAACACCGTGTGCACC
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REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: ROBLINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                              TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                             CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                       AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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                                                                                                                                                                                                                                                                                                                GATAGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
AAACAGAACACCGTGTGCACC
                                                                                                   CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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LOCATION: 1..!
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                                                                                                                                                                                                                                                                                                                                                                   380;
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Similarity 99.7%;
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California
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Pred. No. 2.43e-274;
0; Mismatches 1;
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US-08-050-319B-3 STANDARD; DNA; UNC;

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LOCATION: 1..372
Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;
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              241
                                                          181
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                                                                                         121 GAGTGTGAGAGCGGCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC
                                                                                                                              411
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                                                                                                                                       61 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 120
                                                                                                                                                                                                                                  Local
                                                                                                                                                                                     1 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 51:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                APPLICATION NUMBER:
FILING DATE: 10-May
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
             ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG
                                                                              GAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC
                                                                                                                           CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG
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LENGTH:
                                                                                                                                                                                                                     371;
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Similarity 99.7%;
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                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                          372 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 Bryant Street
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                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                     double
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Pred. No. 3.96e-267;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08273411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Falk, Per
APPLICANT: Gordon, Jeffrey I.
APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Animal model for Gastro-Intestinal
TITLE OF INVENTION: Disease
                                                                                                                                                                                               TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2771 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    711 AACACCGTGTGC 722
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                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                               PUBLICATION INFORMATION:
AUTHORS: Seeburg, et al.
                                                                                                                                  ANTI-SENSE:
                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                    PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                               AUTHORS: Sweetser, et al JOURNAL: Genes & Dev.
                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 30309-4530
                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Atlanta
STATE: Georgia
                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                    JOURNAL:
                                                     RELEVANT RESIDUES IN SEQ ID
                                                                                                                                                                                      nucleic acid
                                                                 1988
239-249
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                                                                                                                                                                                                            Sequence 49, Application US/08050319B Patent No. 5633145
                                                                                                                                                                                                                                       Sequence 49, Application US/08050319B
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                                                                                                                                                                                               Patent No. 5633145
GENERAL INFORMATION:
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AUTHORS: Sweetser, et al
JOURNAL: J. Biol. Chem.
VOLUME: 261
PAGES: 5533-5561
DATE: 1986
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               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version
CURRENT APPLICATION DATA:
                                                                                                                                    APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                              STREET: 635 Bryant
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                       TCCCTCTGTTGCCCTGTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG
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APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                           TCCCTCTGTTGCCCTCTGGTTTCTCCCCCAGGCTCCCGGACGTCCCTGCCTCCTGGCTTTTG
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                                                                               ZIP: 94301
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1 Similarity 97.6%; Pred. No. 8.84e-213;
330; Conservative 0; Mismatches 4;
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                                                                                                                    635 Bryant Street
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                                                                                                      Patent No. 5661132
GENERAL INFORMATION:
                                                                                                                                              Sequence 3, Application US/08343401A
                                                                                                                                                                  01-JAN-1900
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APPLICANT: Andree, Christophe TITLE OF INVENTION: Improved with the control of th APPLICANT: Swain, William F
APPLICANT: Macklin, Michael D
APPLICANT: Eriksson, Elof
APPLICANT: Andree, Christophe

Wound

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET:

PO Box 2113

Quarles & Brady

Madison : WI

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RESULT
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Best Local :
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US-08-343-401A-3 STANDARD;
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Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBDINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                              TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC
                                                                    CGAGTGTGTCTCCTGT 420
                                                                                                                           CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: don TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                      CGAGTGTGTCTCCTGT
                                                                                                            ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                      308;
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Similarity 97.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
DNA; UNC; 4283
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Pred. No. 3.47e-211;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 474;
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Best Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,401A
FILING DATE: 22-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
US-08-445-265A-1 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 713...1049
Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
                                                                        1012 GCCTGCTCTGCCTGGCTTCAAGAGGGCAGTGCC 1049
                                                                                                                                                                                                                                                                                                                   713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
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Local Similarity 95.3%;
hes 322; Conservative
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INFORMATION FOR SEQ ID NO: 3:
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NAME/KEY: sig_peptide
LOCATION: 713...1049
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LENGTH: 4283 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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MOLECULE TYPE: I
IMMEDIATE SOURCE:
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                                                GCCTGCTCTGCCTGCCTTCAAGAGGGCAGTGCC 344
                                                                                                 TCCCTCTGTTGCCCTGTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG
                                                                                                                                                                           GGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCCGGC
                                                                                                                                                                                                                           TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
                                                                                                                                                                                                                                                                                                     ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
713..721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
981..1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(713..721,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                      Score 301; DB 7; Length 4283; Pred. No. 5.54e-212; 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        981..1253)
4283 BP
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                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                     TELEFAX: 608-251-9100 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4283 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                   LOCATION: join(713...721, 981...1250)
Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08445265A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08445265A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION NUMBER: US/08/445,265/
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 604
ATTORNEY_AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Erikss
                                                                                    713 ATGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGGG
 247
                                            187
                                                                                                                                             772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGGTTCTGAATGTGAG
                                                                                                                                    67 TAGCGACCTGTAGATGGGACGGGGGCACTAACCCTGAGGTTTGGGGCTTCTGAATGTGAG
                                                                                                                                                                                                                        / Match 25.0%;
Local Similarity 95.3%;
les 322; Conservative
                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "plasmid DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Eriksson, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
           TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG
GGAGAGAAAAAACAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGGC
                                                                                                                                                                              ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGGAGAGG
                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Madison
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                                                                                                                                                                                                                       Score 301; DB 7; I
Pred. No. 5.54e-212;
0; Mismatches 15;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 53, Application US/08050319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5633145
GENERAL INFORMATION:
                                                                                                               121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 53
SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
                         241
                                                  405
                                                                          181
                                                                                                  345
                                                                                                                                                Y Match 21.2%;
Local Similarity 98.9%;
nes 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Modified human TNFalpha (Tumor TITLE OF INVENTION: Necrosis Factor alpha) Recepton NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: M.Feldmann, P.W. Gray, APPLICANT: M.J.C. Turner, F.M Bre
                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                    MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
                                                           AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTGCTCTGCCTGCCTTCAAGAGGGCAGTGCC
                                                                                                GATAGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404
                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
                                                 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3, Application US/08050319B 5633145
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635 Bryant Street
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                                                                                                                                            Score 255; DB 7; Len;
Pred. No. 2.07e-175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F.M Brennan
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GENERAL INFORMATION:
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US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP
                                                                                                                                     LOCATION: 1..459
Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
                                       602
                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
           300 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 359
                                                  240 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 CGGGACACCGTGTGTACCTGC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                Match 14.18;
Local Similarity 100.08;
                                                                                                                                                  FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/OFFILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBbins, Roberta L
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGACACCGTGTGTGGCTGC 605
                                       CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG
                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                   NAME: Robbins, Roberta L. REGISTRATION NUMBER: 33,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
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                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9430
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635 Bryant Street
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                                                                                    Score 169; DB 7; L
Pred. No. 1.03e-107;
0; Mismatches 0;
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RESULT
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Matches 10
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FILING DATE: 07-JUL-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION: 186
NAME: KUDOVCLK, RODALD J.
REGISTRATION NUMBER: 25/401
REFERENCE/DOCKET NUMBER: 15873005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-6300
TELEFAX: 202-466-2006
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORCANISM: Homo sapiens
DEVELOPMENTAL STAGE: Adult
Sequence 138 BP; 24 A; 51 C; 42 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08086915
Patent No. 5444167
GENERAL INFORMATION:
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US-08-086-915-2 STANDARD; DNA; UNC; 138 BP.
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360 CACCIGCCAIGCAGGITICCITICTAAGAGAAAACGAGIGIGIGICTCCCIGI 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAAACACCGTGTG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGT 770
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 138 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pettersson, Kim SI
TITLE OF INVENTION: Variant Luteinizing Hormone Encoding DNA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1140 Conr
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Adduci, Mastriani, Schaumberg & Schill STREET: 1140 Connecticut Avenue, N.W., Suite 250
                                                                                                                                                                104;
                                                                                                                                                                                 similarity 99.0%;
                                                                                                                                                                Conservative
                                                                                                                                                                                 Score 103; DB 5; Length 138; Pred. No. 5.77e-57;
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Search completed: Wed May 6 10:31:18 1998 Job time: 142 secs.

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John F	<u> </u>
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.	
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Unit	
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MPsrch\_nn n.a. • n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Wed May 6 12:20:06 1998; MasPar time 1075.89 Seconds 1491.095 Million cell updates/sec

Title: >US-08-804-166-1 (1-1049) from US08804166.seq 1049

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 TCCACATGGCTACAGGTAAG.........AGGTGTACCGATGTCCATTC...... .TTATTATCACAAATCTTAAG 1049

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

436399 segs, 764661465 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:em\_in 2:em\_or 3:em\_om 4:em\_ov 5:em\_pl 6:em\_htg
7:em\_hum1 8:em\_hum2 9:em\_ba 10:em\_ro 11:em\_un 12:em\_vi
13:em\_pat

Database:

14:gb\_ro 15:gb\_om 16:gb\_ov 17:gb\_in 18:gb\_pl 19:gb\_ba 20:gb\_st 21:gb\_vi 22:gb\_ph 23:gb\_sy 24:gb\_un 25:gb\_pat 26:gb\_htg 27:gb\_pr1 28:gb\_pr2

Statistics: Mean 11.026; Variance 4.973; scale 2.217

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score 424	Query Match	Query Match Length DB 40.4 483 25	DB 255	ID A29099	Description Synthetic DNA for TNF-	Pred. No
ωN	424 424	40.4	510	25 25	A21525 A20257	oligonucleotide probe. Synthetic nucleotide s	probe.
4	424	40.4	1331	25	A29103	H.sapiens mRNA	mRNA for TNF
<sub>U</sub>	424	40.4	1368	25	A29098	Synthetic DNA for TNF-	or TNF-
σ	424	40.4	2050	27	HUMTNFRP	Human tumor necrosis	crosis f
7	424	40.4	2062	25	I43805	Sequence 24 from pater	m paten
8	424	40.4	2062	25	A21522	TNF alpha gene.	
9	424	40.4	2087	27	HUMTNER	Human tumor necrosis	rosis f
10	424	40.4	2111	27	HUMTNFRB	Homo sapiens tumor nec	mor nec
11	424	40.4	2111	25	A26412	cDNA for (55kD TNF-BP	TNF-BP)
12	424	40.4	2112	27	HUMTNFRC	Human tumor necrosis	rosis f
13	424	40.4	2161	27	HSTNFR1A	H.sapiens TNF-R mRNA	mRNA f
14	424	40.4	2175	25	A43873	Sequence 1 from Patent	Patent

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	<u>3</u>	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15
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n chorionic s	Ř		Sequence 2 from Patent	Human chorionic somato	Human chorionic somato	Synthetic nucleotide s	Sequence 53 from paten	Human messenger RNA fo	Sus scrofa p55 TNF rec	Sequence 3 from patent	Human growth hormone g	Sequence 5 from patent	Human growth hormone (	Human germ line gene f	Sequence 1 from Patent	Sequence 49 from paten	Synthetic nucleotide s	Felis catus tumour nec	Æ	=	3	o D	rom I	Sequence 56 from paten		ot de	47	£	c nucleo	Sequence 1 from patent
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TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC	AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC	AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC	GATAGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC	GATAGTGTGTGTGCCCCAAGGAAAATATATCCACCCCCCAAAATAATTAGTTGGATTTGCTGTACC	Similarity 25; Conserv	130 a	× 11× ×			Patent: EP 0393438-A 49 24-OCT-1990; BOEHRINGER INGELHEIM INTERNATIONAL G	TNF-receptor, TNF-binding protein and	auptmann, R.,	unclassified.  1 (bases 1 to 483)	unidentified	unidentified.	00000		Synthetic DNA	A29099
AGCGGC	ACCTAC	ACCTAC	CAAGGA	CAAGGA	40.4%; 99.8%; 7ative	xret=" 124 c	xref-" 483 anism-	400	tion/Q	93438-	TNF-b	Himmler, A.,	0 483)					for	483 bp
TCCTTC	TTGTAC	TTGTAC	AAATAT	AAATAT	Score Pred 0;	/db_xref="taxon:29278" 124 c 123 g	/db_xref="taxon:32644" [483 [483	1	Location/Qualifiers	A 49 2	inding							NF-bino	P DNA
ACCGCT	AATGAC	AATGAC	ATCCAC	ATCCAC	Score 424; DB Pred. No. 0.00e 0; Mismatches	97278	32644"	*****	ers	RNATIO	prote	Maure						ing p	Ä
TCAGAAAA	TGTCCAGG	TGTCCAGG	CCTCAAAA	CCTCAAAA	DB 25; 0.00e+00 tches	106 t	'db_xref="taxon:32644"  - 483  - 483  - Organism="artificial sequence"	<u>.</u>		0393438-A 49 24-OCT-1990; INGELHEIM INTERNATIONAL G.M.B.H	in and D	Maurer-Fogy, I. and Stratowa, C						TNF-binding polypeptide from patent	
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Eukaryotae; m
Vertebrata; E
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Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stratowa, C.
TNF-receptor; TNF-binding protein and DNA coding therefo
Patent: EP 0393438-A 53 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
                            1 (bases 1 to 1368)
Hauptmann, R. Himmler, A., Maurer-Fogy, I. and Stra
TNF-receptor, TNF-binding protein and DNA coding
Patent: EP 0393438-A 48 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
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407 c 343 g 28
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/organism="unidentified"
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Eutheria; Primates; Catarrhini; Hominidae; H
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Gray, P.W., Barrett, K.J., Chantry, D., Turner, M. and Feldman, M. Cloning of human tumor necrosis factor (TNF) receptor cDNA an expression of recombinant soluble TNF-binding protein Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
                                                                                                       Draft entry and computer-readable sequence for Sci. U.S.A. (1990) In press] kindly submitted by P.W.Gray, 13-AUG-1990.
                                                                                                                                                                                                                                                                                             g339759
TNF receptor; transmembrane receptor;
                                                                                                                                                                                                                                                                                                                             Human tumor necrosis M60275 M37764
                                                                                                                                               Proc. Natl.
91017509
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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/db_xref="taxon:29278"
424 c 375 g 276 t
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155. .274
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155. .1516
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143805
                                  Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,
TNF.alpha. receptor-derived binding protein
Patent: US 5633145-A 24 27-MAY-1997;
Location/Qualifiers
                                                                                                                                Unknown
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/gene="TNF
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FFGLCLLSLLFIGLMYRYQRMKSKLYSIVCGKSTPEKEGELEGTTTKFLAPNPSFSPI
FFGLCLLSLLFIGLMYRYQRMKSKLYSIVCGKSTPEKEGELEGTTTKFLAPNLASDPI
PGFTPTLGFSTVPSSTTTFGSCFUFFAAPRREYAPPTQGADFILATALASDFI
GGCLTCAGSTVPSSTTTSSTTTATVAVVENVPPLRMKEFVRRLGLSDHEIDRLELQN
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        /db_xref="pid:9579600"
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/db_xref="taxon:9606"
155. .1522
PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLKWKEFVRRLGLSDHEIDRLELQN
                                                                                                                                                        /gene="TNF alpha gene"
155. .1522
                                                                                                                                         /gene="INF alpha gene"
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Eutheria; Primates; Catarrhini; Hominidae; H
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Matches 42
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Gatanaga, T., Granger, G.A.,
Goeddel, D.V.
                                                                                                                                                                                                                                                              cell surface receptor; Human placenta, cDNA to
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361-370 (1990)
/db_xref="PID:q339745"
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                                                                           /organism="Homo sapiens"
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                                             /codon_start=1
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Loetscher, H., Pan, Y.-C.E., Lahm, H.-W., Gentz, R., Brockhau Tabuchi, H. and Lesslauer, W. Molecular cloning and expression of the human 55 kd tumon factor receptor
                                                                                                                                                                                                                                                                                                                  g339753
tumor necrosis factor receptor.
Human cell line HL60, cDNA to m
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FFGLCLLSILFIGLMY RYQRWKSKLYSIVCGKSTPEKEGLEGTTYK PLAPNPSESDT
PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPLAPQGADPILATALASDPI
PNPLQKWEDSAHKPQSLOTDDPATLYAVVENVPPLRWKEFVRRLGLSDHELDRLELQN
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187. .273
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/gene="TNF receptor"
/product="tumor necro
187. .1554
                                                                                                                                     Location/Qualifiers
                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 0.00e+00;
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RESULT
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Local Similarity 99.8%;
hes 425; Conservation
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1 (bases 1 to 2111)
Brockhaus, M., Dembic, Z.,
Schlaeger, E.J.
                                                                                                                          patent EP0417563.
A26412
g904968
                                                                     unidentified unidentified
                                                                                                                                                                              cDNA for (55kD TNF-BP)
                                                    unclassified.
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/db_xref="pin:9339754"
/db_xref="pin:9339754"
/translation="MGISTVPDLLPHVLLEILVGIYPSGVIGLVPHLGDREKRDSVC
POGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
SKCRKEMGQVEISSCTVDRDTVCGCRKNOYRHYWSENLFQCFWCSLCLNGTVHLSCQE
KQNTVCTCHAGAFFLRSMECVSCGNKKSLESTRICLFQDIENVKGTEDSGTTVLLFVGI
KQNTVCTCHAGAFFLRSMECVSCGNKKSLESTREKCHADIENVKGTEDSGTTVLLFVDI
FFGLCLLSLIFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
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274. .1551
/gene="TNF receptor"
/product="tumor necrosis factor
2 629 c 587 g 450 t
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GRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
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/note="55 kDa"
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Pred. No. 0.00e+00;
0; Mismatches 1
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                Gentz, R.,
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                Lesslauer,W.,
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                  Loetscher, H.
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Best Local
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1 Similarity 99.88;
425; Conservet
Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 2112)
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g339755
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Patent: EP 0417563-A 24 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
                                                            tumor necrosis factor
Human cDNA to mRNA.
                                                                                                                                        Human tumor necrosis
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//db_xref="55 kD TNF-BP"
//db_xref="55 kD TNF-BP"
//db_xref="pid:9904969"
//taniletonecresssftasenhlerclsc
POGKY.HPQNNSICCTKCHKGTYLYNDCPGPQDTDCRECESGSFTASENHLERCLSC
SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVGOTEDSGTTVLLPLVI
FFGLCLLSLFIGLMYRYGNWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPPNFFSPT
PGFTPILGFSPVPSSTFTSSSTTTPGDCPNFAAPRRYAPPYGCADPILATALASDPI
PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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187. .1554
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Pred. No. 0.00e+00;
0; Mismatches 1
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Best Local Similarity 99.8%;
Matches 425; Conservative
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 TCCTGT 769
                                                                     TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                              TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                                                                                      CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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                                  TCCTGT 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himmler, A., Maurer-Fogy, I., Kroenke, M., Scheurich, P., Pfizenmaier, K., Lantz, M., Olsson, I., Hauptmann, R., Stratowa, C.
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GRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
207. .293
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632 c 589 g 456 t
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Pred. No. 0.00e+00;
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Local Similarity 99.8%;
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                                                                      AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R., Aderka,D., Holtmann,H. and Wallach,D.
Soluble forms of tumor necrosis factor receptors (TNF-Rs). The for the type I TNF-R, cloned using amino acid sequence data of soluble form, encodes both the cell surface and a soluble form
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TNF-R gene; tumor necrosis factor receptor
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KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENKGTEDSGTTVLLPLVI
FFGLCLLSLLFIGLMTRYQRWKSLYSIVCGKSTPEKEELEGTTTKPLAPNPSEST
PGTTPTLGESPVPSGTTTSGSTTSGSTYTFGCCPNFAAPRREVAPPYGGADFLATALSDPI
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GRCLREAQYSMLATWARRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
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2145 2150
/gene="TNF-R"
/note="putative"
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634. .756
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: EP 0657536-A 1 14-JUN-1995;
YEDA RES & DEV (IL)
Other publication ZA 9407962 951121
Other publication JP 7194376 950801
Other publication AU 7574294 950504
Other publication CA 213872 950413.
Location/Qualifiers
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                           AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
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Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
Proteases capable of shedding the soluble TNF-receptor and TNF-R
derived peptides and antibodies against the proteases inhibiting
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larity 99.8%;
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/codon_start=1
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1 641
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/db_xref="taxon:32644"
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Pred. No. 0.00e+00;
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Wallach,D., Brakebusch,C., Varfolomes
Molecules influencing the shedding of
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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129 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 188

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Query Match 40.4%; Score 424; DB 4; L4 Best Local Similarity 99.8%; Pred. No. 2.42e-296; Matches 425; Conservative 0; Mismatches 1;
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Q24441;
Q24441;
O5-NOV-1992 (first entry)
Encodes truncated TNF-alpha 55kD receptor (197 amino acids).
tumour necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
malaria; viral meningits; graft versus host disease;
autoimmune disease; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                            P-PSDB; R24080.

New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.

Example; Fig 7; 43pp; English.

This sequence encodes the designed TNF-alpha 55kD receptor for derivative, as present in pTNFRecd. This was produced as described in 024441. This derivative lacks the 81 carboxyl terminal residues of the cytoplasmic domain. The derivative could be used in the regulation of TNF-alpha mediated responses by binding and sequestering human TNF-alpha e.g. in the treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis, graft versus host disease and autoimmune diseases, esp. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
W09207076-A.
30-ARR-1992.
18-OCT-1991; GB-022648.
18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS SUNLEY RES CENT.
Brennan FM, Feldmann M, Gray PW, Turner MJC;
PSTEEL 52466/20.
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Sequence 608 BP; 148 A; 159 C; 165 G; 136
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                                                  DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanismsm to TNF action Disclosure; Fig 1(1-3); 51pp; German.

CE pTNF-BP15 is one of 30 positives clones in a screened cDNA library from induced TNF-induced fibrosarcoma cells. A TNF-BP had been isolated from the urine of patients with uraemia and probes/primers were constructed from the determined amino acid sequence.

To produce a vector expressing a soluble form of TNF-binding protein, this plasmid was cut with XmmI, amplified by PCR and the amplified DNA cut with BamHI and EcoRI.

The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19 (BRL) cut with the same enzymes to recover pTNF-BP. This was cut with BamHI and EcoRI, and the recovered fragment inserted into pDAD-CNF1 (D05283) to give the required plasmid pADTNF-BP.

See also Q05283 to give the required plasmid pADTNF-BP.

Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T;
  Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                             (BOEH ) BOEHRINGER INGELHEIMINT.
Hauptmann R. Himmler A, Maurer-Fogy I, Stratowa WPI; 90-321987/43.
                                                                                                                                                                                                                                                                                                                     24-OCT-1990.
06-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor pTNF-BP15; ss. Homo sapiens
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Q06282;
29-JAN 1991 (first entry)
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EP-393438-A.
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  l Similarity
425; Conser
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 40.4%;
llarity 99.8%;
Conservative
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213..1325
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 Score 424; DB 1; L
Pred. No. 2.42e-296;
0; Mismatches 1;
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; TNF-BP; TNF-receptor;
                        Length 1334;
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26-MAR-1993; U02938.
30-MAR-1992; US-860710.
(IMMY) IMMUNEX CORP.
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/*tag= c
W09319777-A.
         New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Disclosure; Page 57-59; 85pp; English.
The sequences given in Q49931-32 encode human tumour necrosis factor receptor (TNF-R) and the sequences in Q4993-34 encode human interleukin-1 receptor (TL-TR). These sequences were used in the production of a fusion protein which conformed to one of the formulae:
                                                                                                                                                                                                                                                                                                                                                    Lambda-derived TNF-R cDNA.

Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-1R; fusion protein; linker; TNF, IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft verses host disease; sepsis; inflammation; allergy; autoimmune dysfunction; ss.
                                                                                                                                        Smith WPI; 9
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049932 standard; cDNA to mRNA; 1368
049932;
                                                                                                                           WPI; 93-336592/42.
P-PSDB; R42059.
TNF-R-linker-TNF-R-linker-IL-1R
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Best Local S
Matches 42
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292 A; 424 C; 376 G; 276 T;
                      /*tag= a
/product= hu
mat_peptide
/*tag= "3"
mat_peptide
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                                                                                                                                                                                                                                                                        Q24440 standard; DNA; 2062 BP.
Q24440;
Q5-NOV-1992 (first entry)
Encodes TNF-alpha 55kD receptor.
tumour necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection;
malaria; viral meningits; graft versus host disease;
                                                                                                                                                                                                                                   autoimmune di
Homo sapiens.
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larity 99.88;
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Pred. No. 2.42e-296;
0; Mismatches 1;
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first three cysteine-rich subdomains of TNF alpha receptor for

treating autoimmune disease,

SC laim 4; Fig 1; 43pp; English.

Claim 5; English.

Claim 6; Fig 1; 43pp; English.

Claim 6; Fig 1; 43pp; English.

Claim 7; Fig 1; 43pp; English.

Claim 8; Fig 1; 43pp; English.

Claim 9; Eng
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Best Local S
Matches 42
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(CHAR-) CHARING CROSS SUN Brennan FM, Feldmann M, G WPI, 92-167156/20.
P-PSUB; R24000
New polypeptide capable of first three cysteins-----
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/*tag= f
09207076-A.
30-APR-1992.
18-OCT-1991; G01826.
18-OCT-1990; GB-022648.
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See also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monkey COS-7 cells.
also Q24440-51, R24000, R24080-84, 1
ence 2062 BP; 429 A; 618 C;
                                                                                                                ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag
                                                                                                                                                                                           agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATAGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC
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                                                          TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                                                                                                                                                                                                                                                                                                                       tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc
                                                                                                                                                                                                                                                                                                                                                                                                                               AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                          AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
425; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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M, Gray PW, Turner MJC:
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Pred. No. 2.42e-296;
0; Mismatches 1;
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C; 572
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2 G; 443
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                              New tumour necrosis factor alpha binding protein and polypeptide - useful in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid arthritis Disclosure; Fig 1; 25pp; English.

The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obtd. from a human placental CDNA library in lambda gtil using a probe (Q20974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is useful for treating diseases where TNF alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases, specifically rheumatoid arthritis. See also Q20974.

Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T;
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/*taq= c
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15-JUN-1990; GB-013410.
(CHAR-) CHARING CROSS SUNLE.
Feldman M, Gray P, Turner M, Brennan
WPI: 92-043613/06.
P-PSDB; R20787.
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TNF-alpha binding protein gene.
Tumour necrosis factor alpha; autoimmune diseases;
extracellular domain.
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Q20973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encodes the extracellular domain TNF alpha receptor"
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/note= "homologous to probe
/note= 242..751
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                      ttocagtgottoaattgoagcototgootoaatgggacogtgcacototoctgocaggag
                                                                        agctgctccamatgccgamaggamatgggtcaggtggmgmtctcttcttgcmcmgtggmc
                                                                                                                                                                           tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc
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                                                                                                                                                                                                                                                                                            gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc
AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                             AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
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l Similarity 99.8%;
425; Conservative
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Pred. No. 2.42e-296;
0; Mismatches 1;
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Best Local :
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16-JUL-1999; US-381080.
18-JUL-1989; US-381080.
11-DEC-1989; US-450329.
07-FEB-1990; US-479661.
(SYNE-) SYNERGEN INC.
WPI; 91-073847/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor inhibitor - for suppression of TNF-alpha and -beta, useful as therapeutic agent.

Disclosure; Fig 21; 142pp; English.

The sequence encodes the entire 30 kD TNF inhibitor. The clone from which the sequence was obtd. was isolated from a CDNA library prepd. from RNA form U937 cells treated with PMA-VPHA. The whole gene can be inserted into expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAY-1991 (first entry)
30kD TNF inhibitor precurs
Tumour necrosis factor; in
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Sequence 2088 I
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AU9058976-A.
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                                                                                                                                                                                                                                 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac
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                                            TCCTGT
                                                                                                                                        TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
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BP; 439 A; 63
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factor; inhibitor; ss.
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Pred. No. 2.42e-296;
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CDNA;

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RESULT 7

RESULT 7

ROUNTS stands
AC 010955;
DT 24-MAY-1991
DE Encodes fuman
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KW Tumour Necroo
KW Tumour Stage
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PN 20-MAR-1991;
PR 12-SEP-1989;
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Best Local :
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31-AUG-1990; 116707.
12-SEP-1989; CH-003319.
08-MAR-1990; CH-000746.
20-APR-1990; CH-001347.
(HOFF ) HOFFMANN-LA ROCH
Brockhaus M, Dembic Z, G
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Claim 4: Fig 1; 26pp; German.
Claim 4: Fig 1; 26pp; German.
Partial amino acid sequences were determined for the 55 and 75kD
Partial amino acid sequences were determined primers were
synthesised based on these partial sequences. The primers were used
to produce a cDNA fragment for use as aprobe to screen a human
placental cDNA bank constructed in lambda gtil. Positive clones were
identified and sequenced. DNA constructs comprising the TNF-BP coding
sequence may also contain a fragment encoding a human Ig domain.
Recombinant constructs are used to transform cells to confer
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Encodes human 55kD TNF-binding proteins; s
Tumour Necrosis Factor; binding proteins; s
autoimmune glomerulonephritis; lymphokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    improved TNF-binding
See also Q10956.
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WPI; 91-081851/12.
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EP-417563-A.
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ttocagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag
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                                                                                                                                                                 CGGGACACCGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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                                                                                                                                                                                                                                                                                                                                                   TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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425; Conser
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llarity 99.8%;
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Pred. No. 2.42e-296;
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Best Local S
Matches 42
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06-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1999; DE-920282.
(BOCH ) BOEHRIWGER INCELHEIMINT.
(BOCH ) BOEHRIWGER INCELHEIMINT.
Hauptmann R, Himmler A, Maurer-Fog
WPI; 90-331987/43.
P-PSDB; R07451.
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Q06285 standard; I
Q06285;
29-JAN-1991 (firs
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/label=huTNF-R
EP-393438-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanismsm to TNF action Disclosure; Fig 91(1-2); 51pp; German. ranNF-R8 (Q06584) was used to screen the HS913T cDNA library LambdaTNF-R2 encodes the complete human TNF-R2 and was used construct a plasmid (pad7NF-R) expressing the product the sa pad7NN-BP (see Q06282).

See also Q06382-Q06285.
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Human Tumour Necrosis Factor-Receptor cDNA insert.
Tumour necrosis factor binding protein; TNF-BP; TN
lambdaTNF-R2; raTNF-R8; ss.
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                                                                                                       tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc
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TCCTGT
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425; Conser
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Pred. No. 2.42e-296;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                       CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.

CC Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shedding of the extracellular cc inducing agents, e.g. phorbol myristate acetate (PNA), depending on cell type. The only region of the receptor whose structure affects the cshedding response is the spacer region (see R75012) in the extracellular domain. This region is located close to a site of cleavage of the complete, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras cc subjected to deletion mutations (R75013-25) and substitutions cc subjected to deletion mutations (R75013-25) and substitutions cc side chain identity of these residues, with the acception of the most important residues are conformation of the protein adversely effect the shedding of the receptor is independent of the conformation of the protein adversely effect the shedding process. The mutations shown in R75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNR-R fragments of these inhibitors can be seen in cc managened and the function.

Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;
                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antagonising deleterious effects of TNF. Disclosure; Fig 1; 40pp; English.
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11-CCT-1994; 075742.
12-CCT-1993; IL-107268.
(YEDA ) YEDA RES & DEV CO LTD.
(YEDA ) YEDA RES & DEV CO Varfolomeev E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "possible poly-A signal"
AU9475742-A.
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Q90513;
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                     556
                                                     464
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Local Similarity 99.8%;
hes 425; Conservative
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                                              sapiens.
                                                                                                                AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
                                                                                                                                                                                               gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
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Pred. No. 2.42e-296;
0; Mismatches 1;
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Improved process for the selection of recombinant host cells expressing high level of a desired product - uses eukaryotic host cells contg. a DNA construct comprising a selectable gene Example 2; Page 36-42; 137pp; English.

A dicistronic vector (T15930) comprises a regulatory region cerived from the cytomegalovirus immediate-early gene, a selectable dihydrofolate reductase gene positioned within an intron having a 5 wild-type ras splice donor site, a downstream sequence coding for an immunoadhesin, TnFr-IgG, capable of binding tumour necrosis factor, and a poly-A sequence. Transfection of CHO DHFR- cells and subsequent methotrexate amplification and growth of the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5 cug/ml (15-fold higher compared to conventional vector amplified
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T15931 standard; 1
T15931;
20-JUN-1996 (fir
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28-JUL-1995; U09576.
05-AUG-1994; US-286740.
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WPI; 96-129407/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
WO9604391-A1.
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Recombinant host cell; dihydrofolate reductase; selectable marker;

DHFR; ras splice donor; dicistronic vector; gene expression;

immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                404
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cgggacaccgtgtgtgcgcaggaagaaccagtaccggcattattggagtgaaaacctt
                                                                                                                      tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 1904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gatagtgtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 1784
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                                                                                        AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                            TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523
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Similarity 99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 424; DB 18; 1
Pred. No. 2.42e-296;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1681 G;
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763 795 703 735 643

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RESULTATION OF A PART OF A
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 424; Conser
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10-NOV-1993; 106981.

29-AAY-1993; IL-101769.

(YEDA) YEDA RES & DEV CC

(YEDA) WAILACH D. WAILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q50870;
13.MAY-1994 (first entry)
p55 Tumour necrosis factor receptor coding sequence.
TNF; tumour necrosis factor; receptor; disease; autoimmunity;
rheumatoid arthritis; graft rejection; graft vs. host; septic
effector protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease, septic shock, etc.

Claim 2; Figure 1; 17pp; English.

Modification of the tumour necrosis factor receptor by mutation or Modification of the tumour necrosis factor receptor by mutation or deletion modulates signal transduction and/or cleavage effected by the receptor. This modulation of activity can also be achieved using effector proteins which interact with the TNF receptor or the effector Molecules which interact with the TNF receptor or the effector proteins can be used to treat or prevent diseases associated with TNF activity e.g. autoimmune disease; rheumatoid arthiitis; graft rejection; graft vs. host disease or septic shock. They can also be used to treat overdoses of exogenous TNF.

Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag- a
/product-
EP-568925-
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Q50870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; R42197.
Modulating activity of tumour necrosis factor receptor - u
peptide(s), antibodies, etc. which interact with critical
of receptor or effector protein, for controlling auto-immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2085
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cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt
                                                                      agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac
                                                 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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256..1623
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99.5%;
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Pred. No. 8.37e-295;
0; Mismatches 2;
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repeat_unit 757..858

/*tag= 1
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polyA_signal 2145..2150
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EP-433900-A.
26-JUN-1991.
13-DEC-1990; 124133.
13-DEC-1989; IL-092697.
11-DEC-1989; IL-092697.
12-JUL-1990; IL-095064.
(YEDA) YEDA RES & DEV CO LTD.
Wallach D, Nophar Y, Kemper O, E
Mallach D, Nophar Y, Kemper O, E
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longer"
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Tumour Necrosis Factor; TNF; binding protein; TBP-I;
                                                                                                                                                                                                                                                                                                                        repeat_unit
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/label= soluble_domain
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sig_peptide
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C The Tumour Necrosis Factor Binding Protein I is the soluble for type I TNF receptor and constitutes a fragment of the cell surf. C form of this receptor, corresp. to its extracellular domain. There is no characteristic poly(A) addition signal near the 3' of the cDNA. The sequence ACTANA (tag m) may serve as an calternative to this signal, but with low efficiency.

Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T;
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                                                                                                                                               18-OCT-1991; G01826.
18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS SUBTENDEN FM, FELGMANN M, WPI; 92-167156/20.
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Homo sapiens.
WO9207076-A.
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New poly
                                                                                                                                                                                                                                                                                                                                                                                                         Encodes truncated TNF-alpha 55kD receptor (165 amino acids). tumour necrosis factor alpha; extracellular binding domain; treatment; pulmonary diseases; septic shock; HIV infection; malaria; viral meningits; graft versus host disease; autoimmune disease; rheumatoid arthritis.
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SDB; R24084.

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PS Example; Fig 11: 43pp; English.

Chis sequence encodes the designed TNF-alpha 55kD receptor this sequence encodes the designed TNF-alpha 55kD receptor derivative, as present in pdeeltaIV. This construct was generated by cloning of the BglII/HindIII digested product of a PCR using Cloning of the BglII/HindIII of the Country of th
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05-NOV-1992 (first entry)
Encodes truncated TNF-alpha 55kD receptor (155 amino acids).
Encodes truncated TNF-alpha; extracellular binding domain;
truncated truncatery diseases; septic shock; HIV infection;
malaria; viral meningitis; graft versus host disease;
autoimmune disease; rheumatoid arthritis.
                    18-OCT-1990; GB-022648.
(CHART) CHARING CROSS SUNLEY RES CENT.
GCHART) CHARING CROSS SUNLEY RES CENT.
Brennan FM, Feldmann M, Gray PW, Turner MJC;
WPI; 92-167156/20.
P-PSDB; R24081.
New polypeptide capable of binding human TNF alpha recfirst three cysteine-rich subdomains of TNF alpha rectreating autoimmune disease, septic shock, HIV etc.
Example; Fig 8; 43pp; English.
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18-OCT-1991;
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Q24442 standard;
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  designed
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Pred. No. 2.76e-263;
0; Mismatches 1;
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  TNF-alpha 55kD receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derivative, as present in pdeltaI. This construct was generated by joining PCR fragments by means of overlaps introduced into the primers used for PCR. Gel purified products of PCR's using 5'Cla, IA, IB, and 5D primers were mixed and subjected to further amplification using 5'Cla and 5D as primers. The resulting fragment was digested with ClaI and BglII and cloned into ClaI/BglII digested pTNFRecd, to yield pdeltaI, containing the sequence given. This derivative could be used to regulate TNF-alpha mediated responses by binding and sequestering human TNF-alpha e.g. in the treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral
                                                                                                                                                                                                                                                     Rat Fabpl gut specific promoter and human growth hormone exon 1. Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase; GDP-L-fucose:beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase; alpha 1,2 FT; alpha 1,3/4 FT; tissue-specific promoter; rat liver fatty acid binding protein; transgene; transgent mouse; animal model; intestinal adhesion; Helicobacter pylori infection; stomach; small intestine; gut; epithelial cell; surface receptor; carbohydrate antigen; gastritis; peptic ulcer; neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitis, graft versus host disease and autoimmune diseases, rheumatoid arthritis.

See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
Sequence 474 BP; 110 A; 126 C; 132 G; 106 T;
/number= 1
/note= "Corresponds to nucleotides +3
/note= "Corresponds to nucleotides +3
the human growth hormone (hGH) gene; 1
desirable for cDNA coding for a human
fucosyltransferase to be inserted into
exon 1 of the hGH gene"
                                                                                                                            /*tag= a
/note= "Corresponds to nucleotides -596 to +21
/note= "Iver fatty acid binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                 standard; cDNA; 2771
                                                                                                                                                                                                                             Homo sapiens.
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Location/Qualifiers
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97.8%;
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Pred. No. 8.62e-203;
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Matches 32
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29-APR-1997.
11-JUL-1994;
11-JUL-1994;
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WPI; 97-258275/23.
Animal model for Helicobacter pylori infection - comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.6%;
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Pred. No. 2.90e-201;
0; Mismatches 5;
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed May 6 12:38:32 1998; MasPar time 969.27 Seconds 1315.719 Million cell updates/sec

Description: Perfect Score: N.A. Sequence: Title: >US-08-804-166-1 (1-1049) from US08804166.seq 1049

Comp: 1 TCCACATGGCTACAGGTAAG......TTATTATCACAAAATCTTAAG 1049
AGGTGTACCGATGTCCATTC.....AATAATAGTGTTTTAGAATTC

Scoring table: TABLE default Gap 6

Searched: Nmatch Dbase 0; Query 0 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: embl-est

Database:

1:em\_est1 2:em\_est2 3:em\_est3 4:em\_est4 5:em\_est5 6:em\_est6 7:em\_est8 8:em\_gss 9:em\_est13 genbank-est 11:gb\_est2 12:gb\_est3 13:gb\_est4 14:gb\_est5 10:gb\_est1 11:gb\_est7 17:gb\_est3 13:gb\_est9 19:gb\_est5 15:gb\_est6 16:gb\_est7 17:gb\_est8 18:gb\_est9 19:gb\_est10 20:gb\_est11 21:gb\_sts 22:gb\_est3 23:gb\_est12 24:gb\_est13 25:gb\_est14 26:gb\_est15 27:gb\_est16 28:gb\_est17 29:gb\_est18 30:gb\_est19 31:gb\_est20

Statistics: Mean 11.127; Variance 1.959; scale 5.680

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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248 245	251 251 250	256 256	258 257	258 258	258 258	Score
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H03289 HUM530G10B	C17142 C18403 R77385	R23843 H00781	R71429 H00861	R76249 C17209	HUM505B08B C18240	IJ
	Human placenta cDNA 5' Human placenta cDNA 5' yi75dll.rl Homo sapien	yh48c04.rl Homo sapien yj30d01.rl Homo sapien	y151d03.rl Homo sapien yj31h01.rl Homo sapien	yi72b05.rl Homo sapien Human placenta cDNA 5'	Human placenta cDNA 5'	Description
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ALIGNMENTS	N40676					R68866															HUM50	R23095	R79875				н00795	R65664	H47149	C17966	AA779136	C18044
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	COMMENT	TITLE JOURNAL	REFERENCE AUTHORS	TITLE JOURNAL		REFERENCE AUTHORS	ORGANISM	SOURCE	NID KEYWORDS	DEFINITION	RESULT 1
Tsutomu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co.,Ltd 463-10 kagasuno Kawauchi-cho Tokushima, Tokushima 771-01 Japan Phone: 0886-65-2888	Fujiwara, Otsu Co.,Ltd; 463-1 Japan (Tel:088 Submitted (30-	Direct Submission Submitted (30-MAY	<pre>2 (bases 1 to 373) Fujiwara,T.</pre>	Unpublished(004) Unpublished (199	Okuno, S., Ozaki, K., Shi Takaichi, A., Takeda, S., Maekawa, H., Shin, S. and	Homo.  1 (bases 1 to 373)  Fujiwara,T., Hirano,H.,	Homo sapiens Eukaryotae; mi Vertebrata; Ma	Homo sapiens c mRNA (#6518).	g968208 g968208 EST; EST(expressed known(May 29,1995).	Human placenta cDNA 5'-end GEN-505B08.	HUM505B08B
r Fujiwara GEN Research Institute Pharmaceutical Co.,Ltd kagasuno Kawauchi-cho Lma, Tokushima	ka GEN Res 0 Kagasunc 6-65-2888, May-1995)	ion MAY-1995)	373)	4) 995)	shi 'S.' and	373) irano, H.,	tochondria mmalia; Eu	DNA to mRN	ssed seque	cDNA 5'-e	373 bp
td cho	Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 7 Japan (Tel:0886-65-2888, Fax:0886-37-1035) Submitted (30-May-1995) to DDBJ by:	Direct Submission Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases.			Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.	Katagiri,T., Kawai,A.,	Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;	CDNA to mRNA, clone_lib:Clontech human	sequence tag); Human placenta; similar to	nd GEN-505B08.	mRNA
	Otsuka Pha Tokushima, 35)	L/GenBank (			Y., Shinon kahashi,E.,	wai,A., Kuç	etazoa; Cho s; Catarrhi	ontech huma	placenta;		EST
	Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel.0886-65-2888, Fax:0886-37-1035) Submitted (30-May-1995) to DDBJ by:	databases. Tsutomu			niya,H., Hirai,Y.,	Kuga,Y., Nagata,M.,	ordata; .ni; Hominidae;	nn placenta polyA+	similar to		21-MAY-1996

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2. (bases 1 to 379)
                                                                                                                                                                   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd: 463-10 Ragasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human placenta
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Similarity 99.2%;
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                                                                                               Tel: 314 286 1800
Email: estéwatson wustl.edu
Email: estéwatson wustl.edu
High quality sequence stops: 328
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
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EST.
                                                                                                                                                                                                                             Contact: Wilson RK
WashU-Merck EST Project
Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteicht Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theri Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 392)
Hiller, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M., Holman, M., Hutman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
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Query Match Best Local Similarity

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                                                                                                                  TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846
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2 (bases 1 - 1996)
                                                                                                                                                                                                                                                                                                                                                     Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
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/clone="541F08"
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Pred. No. 0.00e+00;
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to mRNA, clone:541F08
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GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 229
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                                                                   TCAGTGCATGGGCTGCTGCTTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 169
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hakkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, B.
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EST.
                                                                                                                                                                                                                                                                                                                                           High quality sequence stops: 386 Source: IMAGE Consorthum, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consorthum (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Washington University Sch
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
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GLYCOPROTEIN
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                                                                                                                                                                   24.6%;
ilarity 99.2%;
Conservative
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/clone="142757"
114 c 98 g 13
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                                                                                                                                                                   Score 258; DB 11;
Pred. No. 0.00e+00;
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Best Local Similarity 98.9%;
Matches 259; Conservative
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The WashU-Merck EST F
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1 (bass 1 to 423)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stops: 344
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashIngton University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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Best Local :
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GLYCOPROTEIN
R23843
                                                                                                                                                                                                                                                                   Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 334

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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1 (bases 1 to 433)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                    h 24.4%;
Similarity 98.1%;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846
                                          TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 103
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                                                                                                                                                                                                                                                                                                WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trevaskis, E., Waterston, R., Wilson, R.
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                                                                                                                                                                                                                                      High qality sequence stops: 322 source: IMAGE Consortium, LLNL free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Similarity 99.2%;
258; Conservative
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g1571849
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho. Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., S
Kyuniki,H., Suzuki,M., Takatchi,A., Takeda,S., Watanabe
Maekawa,H., Nakamura,Y. and Takahashi,E.
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Direct Submission
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/db_xref="taxon:9606"
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Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsubmitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsubmara, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                           23.9%;
l Similarity 98.9%;
259; Conservative
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Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimas
Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Maekawa,H., Nakamura,Y. and Takahashi,E.
Otsuka cDNA project
Unpublished (1996)
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/db_xref="taxon:9606"
/clone="561H02"
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87 c 73 g
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Pred. No. 0.00e+00;
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256 ATCACAAATCTTAA 269
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High quality sequence stops: 393
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteicht Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theri Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 458)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, S., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilcon, B., Waterston, R., Williamson, A., Wohldmann, P. and Williamson, A., Wohldmann, P., and Williamson, P., and Williamson, A., Wohldmann, P., and Williamson, A., Wohldmann, P., and Williamson, P., and W
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WashU-Merck EST Project
Washington University Scho
4444 Forest Park Parkway,
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Unpublished (1995)
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Fax: 314 286 1810
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Pred. No. 0.00e+00;
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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/clone="151651"
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Pred. No. 0.00e+00;
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Le,M., Lennon,G., Marra,M.,
., Soares,M., Tan,F.,
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son,A., Wohldmann,P. and
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                                                                                                                                                  TIGITATTATCACAA 1041
                                                                                                                                                                              TTGTTATTATCACAA 301
                                                                                                                                                                                                                                                                   GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA
                                                                                                                                                                                                                                                                                                                             TCAGTGCATGGGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC
                                                                                                                                                                                                           CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 250;
Human placenta cDNA 5'-end GEN-556F06.
C18044
g1579646
EST; EST(expressed sequence tag); Human placenta.
Homo sapiens placenta cDNA to mRNA, clone:556F06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Otsuka Pharmaceutical CO.,Ltd
463-10 Kagasuno Kawauchi-cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsutomu Fujiwara
Otsuka GEN Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (7-Nov-1995) to DDBJ by:
                                                                                          C18044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phone:0886-65-2888
Fax :0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiwara,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tokushima, Tokushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.48;
Similarity 98.08;
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                                                                                          519
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Pred. No. 0.00e+00;
0; Mismatches 5
                                                                                          mRNA
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09-SEP-1996

966

906

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TIGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 106
TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, I Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takadi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.

Large-scale sequencing project at Otsuka GEN Research Institute Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST; EST(expressed sequence tag); Human placenta. Homo sapiens placenta cDNA to mRNA, clone_lib:human
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="human placenta polyA+"
/tissue_type="placenta"
89 c 78 g 93 t
                                                                                                                                                                                                        Length
                                                                                                                                       Indels
                                                                                                                                                                                                           336;
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TITLE
JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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Best Local S
Matches 30
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                                           AUTHORS
                                                                                                                  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAGAGAGAAAAAAGAAAACAGCTCCTGGAACAGGGAGAGTACTGGCCTCTTGCTCTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCGCCATGTAAGCCCAG-TATTTGGCCAATCTCAGAAAGCTCCTCCTCCCTGGAGGGA 184
                                                                                                                                                                                                                                                                                                                                                               TITGCCCTGCTCTGCCTGCCCTGCCTTCA-GAGGCTGCTGCTGCCG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATCGCCATCTAAGGCCAGATATTTGGCCAATCTCTGAATGTTCCTGGTCCCTGGAGGGA 218
                                                                                                                                                                                                                                                                                                                                         TTTGGCCTGCTGCCTGCCTGGCTTCAAGAGGGCAGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                CGGCTCCCTCTGCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAGAGAGA--AAAACAAA-CAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTC 241
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 519)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
                                                                                                                                               z)46hll.sl Soares fetal liver spleen clone 453381 3' similar to gb:V00518 CHAIN PRECURSOR (HUMAN);.
AA779136 g2838467
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A.,
Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., S
Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe
Maekawa,H., Nakamura,Y. and Takahashi,E.
                                                                            Eukaryotae; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Otsuka cDNA project
Unpublished (1996)
                                                                                                               Homo sapiens
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Eukaryotae; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="556F06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="placenta"
140 c 153 g 1
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No. 0.00e+00;
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                                                                                              Mammalia;
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                                                                                            Eutheria;
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JOURNAL
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Best Local Similarity 95.9%;
Matches 255; Conservative
                                                                                                                                                                                                                                                                                       1048
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                                                                                                                                                                                                                                                                                                     253 TTAAGATTTGTGATAATAACAAGTACTGCAGTGGCACGCCGTGTGGGTTCTCCACTTTTGAA 312
808
                    CTG-AGCGTG-ATTCTGGGGAATCTG 516
                                                                                                                                          GACGTTCTTTTGGACCAACATCGTCTTTTGGACCTTAGTGGAGTGGGATATGCTCTAGA
                                                                                                                                                                                                                                 ACCCCCATTACTGTGACCCTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT 372
                                                                                           GAAGCAGCCCATGCACTGAAGTAGTGGGGCACCGGGCTCGTAGAAGAATGGGGGTTTC 492
                                                                                                                                                                                                                                                                                      TTAAGATTTGTGATAATAACAAGTACTGCAGTGGCACCCCGTGTGGTTCTCCACTTTGAA 989
CTGTAGCGTGCATTCTGGGCAACCTG
                                                                   GAAGCAGCAGCCCATGCACTGAAGTATTGGGGCACCCGGCTGGGAGAAGAATGGGTTTTC
                                                                                                                                                                           GACGTTCTTTTGGACCAACATCGTCTTCTTGGACCTTAGTGGAGTGGGATATGCTCTAGA 432
                                                                                                                                                                                                                 ACCCCCCATGACTGTGACCCTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.llnl.gov) for
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 316.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Fórest Park Parkway, Bo
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
98 c 127 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="453381"
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Pred. No. 0.00e+00;
0; Mismatches 9
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783
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:50:59 1998; MasPar time 8.51 Seconds 449.440 Million cell updates/sec

Sequence: Description: Perfect Score: >US-08-804-166-2 (1-256) from US08804166.pep 1994 SRTSLLLAFGLLCLPWLQEG......GFKVENHTGCHCSTCYYHKS 256

Tabular output not generated.

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Searched:

120837 seqs, 14945562 residues

a-geneseq31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 31.442; Variance 119.617; scale 0.263

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Length	BB	Ħ	Description	Pred. No.
_	1994	100.0	256	26	W33357	TBP(20-161)/hCG-alpha	1.90e-207
N	1667	83.6	285	26	W33359	TBP(20-190)/hCG-alpha	
w	1321	66.2	307	26	W33358	TBP(20-161)/hCG-beta	6.46e-132
4	1291	64.7	336	26	W33360	<	
G	1124	56.4	161	G	R27496	Native 30 kD TNF inhi	6.19e-110
0	1124	56.4	199	4	R24080	Truncated TNF-alpha 5	6.19e-110
7	1124	56.4	309	13	R70108	TNF-R-GBPH fusion pro	٠
&	1124	56.4	371	N	R07449	Tumour Necrosis Facto	
9	1124	56.4	451	13	R70107	TNF-R-GBP 130 fusion	6.19e-110
10	1124	56.4	455	œ	R42059	Lambda derived TNF-R.	6.19e-110
11	1124	56.4	455	N	R10986	30kD TNF inhibitor pr	
12	1124	56.4	455	4	R20787	TNF-alpha binding pro	.19e-
13	1124	56.4	455	14	R75084		6.19e-110
14	1124	56.4	455	N	R07451	Human Tumour Necrosis	
15	1124	56.4	455	N	R11082	Human 55kD TNF-bindin	6.19e-110
16	1124	56.4	455	4	R24000	TNF-alpha 55kD recept	.19e-
17	1124	56.4	547	13	R70104	H fus:	6.19e-110
18	1124	56.4	884	13	R70109	TNF-R-GBP 130 fusion	
19	1124	56.4	900	13	R70103	TNF-R-GBP 130 fusion	.19e-

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61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120

Query Match 100.0%; Best Local Similarity 100.0%; Matches 256; Conservative

Score 1994; DB 26; Pred. No. 1.90e-207; 0; Mismatches 0;

Length 256; Indels

0;

Gaps

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21 1124 56.4 1604 13 R70105 TNF-R-EBA 175 fusion 121 1124 56.4 1604 13 R70105 TNF-R-EBA 175 fusion 22 1118 56.1 443 R751032 Mutant p55 tumour nec 23 1118 56.1 445 R751033 Mutant p55 tumour nec 24 1118 56.1 455 R751034 Mutant p55 tumour nec 25 1118 56.1 455 R751034 Mutant p55 tumour nec 26 1110 55.7 455 R751034 Mutant p55 tumour nec 27 1118 56.1 455 R751034 Mutant p55 tumour nec 28 1110 55.7 455 R751034 Mutant p55 tumour nec 29 1110 55.7 455 R751034 Mutant p55 tumour nec 29 788 99.5 461 2 R70450 Type I TWF receptor. 167 33.5 92 1 R75182 MCG/DCG alpha subunit 67 Urina 167 33.5 92 1 R75182 MCG/DCG alpha subunit mut 39 667 33.5 116 26 W31665 MCG alpha subunit mut 39 667 33.5 116 12 R75105 Engineered human alph 176 667 33.5 222 15 R86256 Single chain gonadotr 177 886254 Single chain gonadotr 178 886251 Single chain gonadotr 178 886247 Single chain gonadotr 178 886248 Single chain gon	_	_	_	4	_	_	w	w	w	w	w	w	tω	w	w	w	N	N	N	N	N	N	N	N	N	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid dimeric protein comprising two co-expressed units - each probased on receptor or ligand and a subunit of a heterodimeric hormone, especially FSH, for inducing follicular maturation PS Example; Pages 37-38; 60pp; English.

CA novel fusion protein comprises 2 dimer forming co-expressed amino CC acid sequences, each consisting of a homodimeric or heterodimeric CC receptor chain or ligand, with ligand-receptor binding activity, CC bound directly or via a peptide linker to a subunit of a CC chain or subunits. The fusion protein each consisting of the funding a heterodimeric CC (hCG-alpha) fusion protein denoted by the present sequence, cc significantly increases the biological activity of the hormone cranes of injections needed.
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Best Local S
Matches 25
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20-FEB-1996; US-011936.
(ISTF) ARS APPLIED RES SI
Campbell RK, Chappel SC, Campbel SC, WPI; 97-425036/39.
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W33359;
19-MAR-1998 (firs
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WO9730161-A1.
21-AUG-1997.
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TBP(20-190)/hCG-alpha fusion protein.
Fusion protein; thrombopoietin; TPO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein; thrombopo alpha subunit; hCG-alpha.
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                    lvqknvtsestccvaksynrvtvmggfkvenhtachcstcyyhks
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Similarity 89.1%;
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Pred. No. 1.11e-170;
2; Mismatches 0;
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Example: Pages 34-35; 60pp; English.

A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric receptor chain or ligand, with ligand-receptor binding activity, bound directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the thrombopoletin (TPO)/human chorionic gonadotrophin beta subunit (hCG-beta) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone component, reducing the requirement for hormone itself and the number of injections needed.
Homo sapiens.

W09730161-A1.

D21-AUG-1997.

D21-AUG-1997; U02315.

F 20-FEB-1996; US-011936.

R 20-FEB-1996; US-011936.

R (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

I Campbell RR, Chappel SC, Jameson BA;

RWPI; 97-425036/39.

R N-PSDB; T94022.

R N-PSDB; T94022.

R N-PSDB; T94022.

T based on receptor or ligand and a subunit of a heterodimeric hormone, especially FSH, for inducing follicular maturation S Example; Pages 39-40; 60pp; English.
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21-AUG-1997.
20-FEB-1997. U02315.
20-FEB-1996; US-011936.
(ISTF ) ARS APPLIED RES SY Campbell RK, Chappel SC, J WPI. 97-445036.99.
N-PSDB: T94008.
Hybrid dimeric protein com
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19-MAR-1998 (first entry)
19-(20-190)/hCG-beta fusion prot
190 (20-190)/hCG-beta fusion prot
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Homo sapiens.
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Similarity 98.8%;
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Pred. No. 6.46e-132;
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                                                                                                                                                                                                                     PT rheumatoid arthritis, septic shock etc.

PS Claim 54; Fig 2; 100pp; English.

CC The sequence shows a native 30 kD TNF inhibitor which may be condified to contain at least one non-native cysteine residue, pref.

CC at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is contained to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols. may be linked via this non-peptidic spacer. The modified polypeptides show improved the construction of the properties, i.e. increased mol. wt. hence reduced collarance rate following s.c. or systemic administration, increased collypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
        Matches
                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYND) SYNERGEN INC.
(SYND) SYNERGEN INC.
Armes IG, Brewer MT, Evans RJ, Kohno T, Thompson RC;
WPI; 92-348933/42.
New ethylene glycolated polypeptide(s) with improved
New ethylene glycolated polypeptide(s) with improved pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric receptor chain or ligand, with ligand-receptor binding activity, bound directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit (hCG-beta) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone number of injections needed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1992.
13-MAR-1992; U02122.
15-MAR-1991; US-669862.
17-JAN-1992; US-822296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour necrosis factor; ethylene glycol; pharmokinetic; adult respiratory distress syndrome; rheumatoid arthrit septic shock; pulmonary fibrosis; spacer.
                                                                                                                                                                   as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis,inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens. 
W09216221-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-1993 (first entry)
Native 30 kD TNF inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmacokinetic properties for treating e.g. TNF and IL-1 mediated diseases, e.g. adult respiratory distress syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R27496 standard;
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                                                                                                                                           See also R27495.
                             56.4%;
99.3%;
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Pred. No. 1.46e-128;
1; Mismatches 0;
Score 1124; DB 5; 1
Pred. No. 6.19e-110;
1; Mismatches 0;
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Best Local S
Matches 14
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18-OCT-1990; GB-022648.
(CHAR-) CCHARING CROSS SU
Brennan FM, Feldmann M,
WPI; 92-167156/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating autoimmune disease, septic shock, HIV etc.

Example: Fig 7; 43pp; English.

This sequence is a truncated TNF-alpha receptor derivative, as en in pTNNRecd. This was produced as described in Q24440.

This derivative lacks the 81 carboxyl terminal residues of the cytoplasmic domain. The derivative could be used in the regulation of TNF-alpha mediated responses by binding and sequestering human TNF-alpha e.g. in the treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis, graft versus host disease and autoimmune diseases, esp. rheumatoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Truncated TNF-alpha 55kD receptor.

tumour necrosis factor alpha; extracellular binding domain; treatment; pulmonary diseases; septic shock; HIV infection; malaria; viral meningits; graft versus host disease; autoimmune disease; rheumatoid arthritis.
                     10-NOV-1995 (first entry)
TNF-R-GBPH fusion protein.
TNF-R-GBPH fusion protein.
Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein blood cell; cytokine receptor; glycophorin binding peptide 130 GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin tumour necrosis factor receptor; TNF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also Q24440-51,
Sequence 199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens W09207076-A.
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R24080 standard;
  Chimeric
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New polypeptide capable
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05-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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larity 99.3%;
Conservative
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                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R24000, R24080-84, R27585, Q29236-8
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M, Gray PW, Turner MJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of binding human TNF alpha - comprises ch subdomains of TNF alpha receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1124; DB 4;
Pred. No. 6.19e-110;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell and PT a receptor peptide.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite (Plasmodium falciparum) peptide (capable of binding to a red blood CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples CC of these hybrid peptides. R70108 is a fusion of tumour necrosis factor CC receptor (in accordance with H Loetscher et al. Cell, Vol. 61, 351-359) CC and glycophorin binding protein (GBP) homologue (GBPH). The CC cytokine receptors not normally found on RBCs means that the CC cytokine receptors not normally found on RBCs means that the CC cytokine can bind harmlessly to the RBC without deleterious effect. CC The RBC protects the hybrid peptides from excretion from the kidney, and CC another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides cused, others include EBA 175 (175 kDa erythrocyte binding to a receptor in CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to CC pref. Glycophorin A, B and C, slalo glycophorteins, found on the surface cytokines in the circulation to reduce pathological damage.
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Best Local :
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R07449 standard;
R07449;
                                                                                                                                         06-APR-1990;
21-APR-1989;
21-JUN-1989;
                                                                                                                                                                                                                                                                                                               29-JAN 1991 (first entry)
29-JAN 1991 (first entry)
Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
Tumour necrosis factor disease; parasitic disease; cachexia;
                                                   21-RPR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT.
Hauptmann R, Himmler A, Maurer-Fogy
WPI; 90-321987/43.
                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                            autoimmune disease; shock.
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WPI; 95-115452/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
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Similarity 99.3%;
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; GB-018350.
; GB-017021.
TNF binding protein and TNF- receptor -
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number"
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be
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Pred. No. 6.19e-110;
1; Mismatches 0;
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                                                                                  Stratowa
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                             PT a receptor peptide.

PS Example A; Page 53-54; 93pp; English.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite CC (Plasmodium falciparum) peptide (capable of binding to a red blood CC (Plasmodium falciparum) peptide are claimed. R70103-25 are examples CC of these hybrid peptides. R70107 is a fusion of tumour necrosis factor CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) CC and glycophorin binding protein (GBP) 130. The use of cytokine can bind CC are protein to the RBC without deleterious effect. The RBC protects the CC receptors not normally found on RBCs means that the cytokine can bind CC hybrid peptides from excretion from the kidney, and due to steric CC hindrance prevents the cytokines binding to a receptor in another cell. CC GBP 130 or GBPH (GBP homologue) are the prefid. malaria parasite peptides used, others include EBA 175 (175 kDa crythrocyte binding antigen), CC PMMSA (pre major merozoite surface antigen) and the Duffy binding CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on CC the surface of RBCs. The hybrid peptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of e.g. COS7 cells. The expressed proteins are useful prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock, cachexia, autoimmune diseases, adult respiratory distress syndrome etc., or side effects of treatment with TNG-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions.

See also Q06282-Q06285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     red blood
GBP 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1995.
01-SEP-1994; G01900.
03-SEP-1993; GB-018350.
23-AUG-1994; GB-017021.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      New hybrid peptide(s) for binding cytokine(s) - malaria parasite peptide capable of binding a re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prendergast KF;
WPI; 95-115452/15.
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Hybrid peptide
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R70107 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d peptide; malaria parasite; Plasmodium falciparum; fusion protein; lood cell; cytokine receptor; glycophorin binding peptide 130; 30; GBPH; glycophorin binding peptide homologue; glycophorin A.
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Similarity 99.3%;
142; Conservative
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    comprising a
red blood cell and

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                             Query Match
Best Local S
Matches 14
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                                                                                                             The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or II-1, particularly in conditions in which both TNF and II-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral mediatia, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and
                                                                                                                                                                                                                                                                                                                                                                              New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Disclosure; Page 57-59; 85pp; English. Disclosure; Page 57-59; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple scierosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft verses host disease; sepsis; inflammation; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R42059 standard;
R42059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune dysfunction.
                                                                                                                                                                                                                                                                                                                                     factor receptor (TNF-R) and the sequences in R42060-61 represent human interleukin-1 receptor (IL-1R). These sequences were used the production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q49932.
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                                                                                                                                                                                                                                                                              TNF-R-linker-TNF-R
                                                                                                                                                                                                                                                                                                         formulae:
TNF-R-linker-TNF-R-linker-IL-1R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-1994
                                                                                                      utoimmune
                                                                                                                                                                                                                                                                                            IL-1R-linker-TNF-R-linker-TNF-R or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
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30-MAR-1992; US-860710.
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26-MAR-1993;
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41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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                                                                                                      dysfunctions
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                              Conservative
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41..455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                            56.4%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mature hTNF-R"
                           Score 1124;
Pred. No. 6.
1; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.19e-110;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165
                              Mismatches
                             :.19e-110;
:ches 0;
                                                          BB
                                                          8,
                                                        Length 455;
                              Indels
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                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                             Gaps
                                                                                                                                                                                                                                                                                                                                                    'n
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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16-JUL-1990;
18-JUL-1989;
11-DEC-1989;
07-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 91-
N-PSDB;
                                                                                                                                            R20787
R20787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and beta, useful as therapeutic agent.

Disclosure; Fig 21; 142pp; English.

The sequence comprises the entire 30 kD TNF inhibitor. The clone from which the sequence was deduced was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA. The whole gene can be inserted into expression vectors for prepn of TNF inhibitor for use in the treatment of inflammatory and approximately and the treatment of inflammatory and the treatment of the sequence was sequenced.
                                                                                     TNF-alpha binding protein. Tumour necrosis factor alpha; extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R10986;
13-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R10986 standard; Protein;
             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degenerative diseases. The See also R10984 and R11001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30kD TNF inhibitor precursor
                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-1989; US-381080.
11-DEC-1989; US-450329.
07-FEB-1990; US-479661.
(SYNE-) SYNERGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU9058976-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                       Homo sapiens.
                                                                                                                                 1-MAY-1992
                                                                                                                                                                                                                     143
                                                                                                                                                                                                                                                 161
                                                                                                                                                                                                                                                                                                        101
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                                                                                                                                                                                                                                                                                          scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
                                                                                                                                                                                                                                                                                                                                     DSVCPQGKY1HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                    dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91-073847/11.
DB; Q10883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                              kqntvctchagfflrenecvscs
                                                                                                                                                                                                                     KONTVCTCHAGFFLRENECVSCA
                                                                                                                                                                                                                                                                            SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
                                                                                                                                                                                                                                                                                                                                                                                               142;
                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                             h 56.4%;
Similarity 99.3%;
142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 AA;
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             058976
            /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40..4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                        Location/Qualifiers
/note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cleavage gives active protein
"mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The active protein is claimed (Claim 8).
                                                                                                                                                           455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455
                                                                                                                                                                                                                                                                                                                                                                                            Score 1124; DB 2;
Pred. No. 6.19e-110;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165
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                                                                                                    autoimmune diseases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for suppression of TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 455;
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Indels

0

Gaps 100 82

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TRESOLT RESOLT RESOLT RESOLT RESOLUTION RESO
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Best Local Similarity
Matches 142; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. rheumatoid arthritis

Disclosure; Fig 1; 25pp; English.

The amino acid sequence is that of tumour necrosis factor alpha
binding protein which contains the extracellular domain of human TNF
alpha receptor. It is soluble and can be used in the regulation of
TNF-mediated responses by binding and sequestering the cytokine. It
can therefore be used therapeutically to treat disorders such as
cachexia, sepsis and autoimmune diseases, specifically rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-1990; GB-013410.
(CHAR-) CHARING CROSS SUNLE.
Feldman M, Gray P, Turner M, Brennan
                                              misc_difference
                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                              modified_site
                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R75084 standard;
R75084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_site
                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New tumour necrosis factor alpha binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   phorbol myristate acetate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 kqntvctchagfflrenecvscs 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in treating cachexia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour necrosis factor receptor; TNF-R; human; murine; chimera;
ermal growth factor receptor; EGF-R; protease; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scskcrkemgqveissctvdrdtvcgcrkngyrhywsenlfqcfncslclngtvhlscqe 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92-043613/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                            /note=
1 202
/note=
203
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145..147
                                                                                          /note=
201
                                                                                                                                                                                                                                                                                                                          /note= "N terminus of 54..56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "potential N-glycosylation site" 151..153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30..199
/note= "extracellular domain"
212..234
                                                                                                                                                                                        193..210
                                                                                                                                                                                                                                    /note= "glycosylation 161..163
                                                                                                                                                                                                                                                                                   145..147
                                                                                                                                                             /note=
                                                                                                                                                                                                            /note-
                                                                                                                                                                                                                                                                                                    /note= "glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.4%;
99.3%;
                                                                                                                                            . 210
                                                                                                                                                             "peptide used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *transmembrane
                   "essential
                                                               "major C terminus for soluble p55 TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "potential N-glycosylation site"
                                                                                                                                                                                                            "glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor;
te; PMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1124; DB 4; I
Pred. No. 6.19e-110;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ha binding protein and polypeptide sepsis and auto immune diseases
                                                                                                                 region
                 for shedding reaction"
                                                                                                                                                                                                                                                        site*
                                                                                                                                                                                                                                                                                                                                                        soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain'
                                                                                                                                                                                                                                                                                                       site"
                                                                                                                                                               creation
                                                                                                                                                                                                                                                                                                                                                   p55 TNF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 455;
                                                                                                                                                             of chimeras*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
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RESULT
ID AC RO
AC RO
DT 25
DT 25
DT 41
KW 11
KW 11
KW 11
KW 21
PD 22
PR 21
PR 41
PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This sequence represents human p55 tumour necrosis factor (TNF-R).

CC Expression of this receptor is regulated by shedding of the extracellular CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell ctype. The only region of the receptor whose structure affects the CC shedding response is the spacer region (see R75012) in the extracellular CC domain. This region is located close to a site of cleavage of the CC molecule, and links the Cys rich module to the transmembrane domain. The spacer region was used to create the chimeras CC between human p55 TNF-R and murine epidermal growth factor receptor CC (EGF-R) that are represented by R75007-11. This spacer region was CC subjected to deletion mutations (R75013-25) and substitutions CC (R75026-47). Of the spacer region, the most important residues are CC (R75026-47). Of the spacer region, the most important residues are conformation of these residues, with the exception of a limited CC enformation of the protein adversely effect the shedding process. CC inhibitors of a protease that is capable of cleaving the soluble TNF-R CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in CC enterior of a protease that is capable of cleaving the soluble TNF-R CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in CC enterior of a protease that is capable of cleaving the soluble TNF-R CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in CC enterior of the protein adversely of these inhibitors can be seen in CC enterior of the protein adversely of these inhibitors can be seen in CC enterior of the protein adversely of these inhibitors can be seen in CC enterior of the protein adversely of these inhibitors can be seen in CC enterior of the protein adversely of these inhibitors can be seen in CC enterior of the protein and the colubration of the protein the colubration of th
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       24-CCT-1990.
26-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YEDA ) YEDA RES & DEV
Batkin M, Brakeh...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R07451
                                                                                                                                                                                                                                                                         Human Tumour Necrosis Factor-Receptor from lambdaINF-R2 cDNA insert. Tumour necrosis factor binding protein; INF-BP; INF-receptor; Infectious disease; parasitic disease; cachexia; autoimmune disease; shock; lambdaINF-R2; raINF-R8.
                                                                                                                                                                                                                                                                                                                                                                                                           R07451;
29-JAN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New protease capable of cleaving soluble tumour necrosis factor (TNF) receptor - from cell-bound TNF- receptor, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 95-194342/26.
N-PSDB; Q90513.
                                                                                                                                                                                                            EP-393438-A.
                                                                                                                                                                                                                                         Homo sapiens.
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12-OCT-1993;
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142; Conservative
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Pred. No. 6.19e-110;
1; Mismatches 0;
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N-PSDB; Q06285.

N-PSDB; Q06285.

DNA encoding TNF binding protein and TNF- receptor - used in PT DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanismsm to TNF action PT tumour treatment and to understand mechanismsm to TNF action PT tumour treatment and to screen the HS913T cDNA library.

CranNF-RB (Q06284) was used to screen the HS913T cDNA library.

CranNF-RB (Q06282) was used to screen the same way to construct a plasmid (pADTNF-R) expressed proteins are useful construct a plasmid (pADTNF-R) expressed proteins are useful as pADTNF-BP (see Q06282). The expressed proteins are useful prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or beta (e.g. infectious or parasitic diseases, shock, cachexia, autoimmune diseases, adult respiratory distress syndrome etc., or side effects of treatment with CTNR-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions.
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Best Local Similarity
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31-AUG-1990; 116707.
12-SEP-1989; CH-003319.
08-MAR-1990; CH-000746.
20-APR-1990; CH-001347.
prodn. ; Fig 1; 26pp; German. Partial amino acid sequences were determined for TNF-BPS (see R11072-R11081) and oligonucleotide synthesised based on these partial sequences. The
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Tumour Necrosis Factor; binding proteins; septic shock;
autoimmune glomerulonephritis; lymphokine; cytokine.
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R11082 standard;
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Insoluble tumour necrosis encoding them, useful in p
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Schlaeger EJ;
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                                                                                                                                                                                                                                 to produce a cDNA fragment for use as aprobe to screen a human placental cDNA bank constructed in lambda gtll. Positive clones were identifed and sequenced. DNA constructs comprising the TWF-BP coding sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer improved TNF-binding properties.
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                                           143
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                                                                                    KQNTVCTCHAGFFLRENECVSCA
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larity 99.3%;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed May 6 08:50:01 1998; MasPar time 11.89 Seconds 786.633 Million cell updates/sec

Description:
Perfect Score:
Sequence: Title: >US-08-804-166-2 (1-256) from US08804166.pep 1994

1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150 Gap 11

Searched: 120446 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 40.411; Variance 71.735; scale 0.563

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

22211111111000000000000000000000000000	Result
1124 11118 11118 11098 1098 841 841 846 847 667 647 548 548 548 548 548 548 548	Score
277.1.1.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4	- 54 - 54
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2.23e-230 5.83e-229 5.14e-228 6.85e-224 3.08e-224 3.08e-192 7.05e-164 7.05e-164 7.05e-1164 7.05e-1164 7.05e-1164 7.05e-1164 7.05e-118 1.99e-118 1.99e-118 1.99e-118 1.99e-118 1.99e-118 1.22e-96 8.89e-96 8.89e-96 1.22e-94 1.22e-94 1.22e-94 1.22e-94	Pred. No.

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FEATURE 68-70 143-145 9-11,19-21 133-136,139-142 27-31,41-44 27-36,85-87 92-98,101-106 113-117,126-129 5-19	rnal le	#Journal #title REFERENCE #authors #journal #title REFERENCE #authors	TITLE tume PDB_TITLE ext.  RORGANISM #f00 #note re #note	RESULT 1 ENTRY
<pre>#region helix (right hand 3-10)\ #region helix (right hand 3-10)\ #region beta sheet\ #region beta sheet\</pre>	Cell (1993) 73:431-445 Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for TNF receptor activation. receptor activation. Resolution: 1.85 angstroms Determination: X-ray diffraction R-value: no refinement binding protein; cytokine; signalling protein	Naismith, J.H.; Devine, T.O.; Brandhuber, B.J.; Sprang, S.R. J. Biol. Chem. (1995) 270:13303 Crystallographic evidence for dimerization of unliganded tumor necrosis factor receptor. TN026252 Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale, K.; Naismith, J.H.; Sprang, S.R. J. Mol. Biol. (1994) 239:332 Two crystal forms of the extracellular domain of type i tumor necrosis factor receptor. A40737 Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld, H.J.; Broger, C.; Leetscher, H.; Lesslauer, W.	or necrosis factor receptor extracellular domain, che racellular domain of the 55kda tumor necrosis factor sceptor. crystallized at ph3.7 in p 21 21 21.  rmal_name Homo sapiens #common_name man ressed in Escherichia coli, the construct contains seldues 12 to 172 of the mature sequence of the entimentation of the contains septor. residue 11 is mutated to met as a result of pression system  solution system  smith, J.H.; Sprang, S.R.  nitted to the Brookhaven Protein Data Bank, July 1990 pdb:leXT	1EXTB #type complete

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Best Local Similarity 99.3%;
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tumor necrosis factor #cross-references MUID:90235285
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                                                                                                                                                     ##residues 1-455 ##label LOE
##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
##experimental_source placenta
##note part of this sequence, including the amino end of the
##note mature protein, confirmed by protein sequencing
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##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;
##CIOSS-TEFERENCE PID:g339750
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##residues 1-45!
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                                                                                                                                                                                                                                                                                                                                Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.;
M.; Tabuchi, H.; Lesslauer, W.
Cell (1990) 61:351-359
Molecular cloning and expression of the
necrosis factor receptor.
                                                           A34900
Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raa. H.; Kohr, W.J.; Goeddel, D.V.
Cell (1990) 61:361-370
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Structure of the human TNF receptor 1 (p60) gene (TNRF1) localization to chromosome 12p13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor necrosis factor receptor type 1 precursor - humanALTERNATE_NAMES tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein 1 (TNF blocking factor) #formal_name Homo sapiens #common_name man 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 24-cct-1997
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Pred. No. 2.23e-230;
1; Mismatches 0;
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#journal
#title
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##molecule_type protein
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#journal EMBO J. (1990) 9:3269-3278
#title Soluble forms of tumor necrosis factor receptors (TNF-Rs).
The CDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.
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#title Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A38281
                                                                                       #title Tumor necrosis factor inhibitor: purification, NH-2-term! amino acid sequence and evidence for anti-inflammatory immunomodulatory activities.

#cross-references MUID:90292116
#accession A60231
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#title
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Pfizenmaler, K.; Lantz, M.; Olsson, I.; Hauptmann, R.
Stratowa, C.; Adolf, G.R.
#journal DNA Cell Biol. (1990) 9:705-715
Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
#cross-references MIID:91090841
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***Cross-references GB:M33294; NID:g339744; PID:g339745

ENCE A36555
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##residues 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
##residues 107-128;162-167,'X',169-201 ##label HI2

##note the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
                                                                                                                                                                                                                                                                                                                               ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-455 ##label NOP
##cross-references EMBL:X55313; NID:g37223; PID:g37224
##note parts of soluble TNF binding protein 1, including
amino and carboxyl ends, were confirmed by prote
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**cross-references GB:M63121;
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##cross-references GB:M37764
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Gene (1993) 134:209-216
Cloning and partial characterization of the promoter human p55 tumor necrosis factor (TNF) receptor JT0758
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#title purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.
#accession A38258
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atrons 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
IFICATION #superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology
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##residues 41-60 #
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Eur. J. Haematol. (1989) 42:270-275
Isolation and characterization of a tumor necrosis
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Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
Amino acid sequence of natural tumor necrosis factor alpha
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J. Biol. Chem. (1995) 270:13303
Crystallographic evidence for dimerization
tumor necrosis factor receptor.
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#formal_name Homo sapiens #common_name man expressed in Escherichia coli, the construct contains residues 12 to 172 of the mature sequence of the entire receptor. residue 11 is mutated to met as a result of the
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Crystal structure of the soluble human 55 kd TNF
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    K.; Naismith, J.H.; Sprang, S.R.
    J. Mol. Biol. (1994) 239:332
    Two crystal forms of the extracellular necrosis factor receptor.

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                                                                                                                                                                                                                                                                                                   R-value: no re
binding
                                                                                                                                                                                                                                                                                                                                        receptor activation.
Resolution: 2.25 and activation.
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Determination: X-ray diffraction
R-value: no refinement
                                                                           h 55.9%;
Similarity 99.3%;
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Similarity 99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.; Naismith, J.H.; Sprang, S.R.
J. Mol. Biol. (1994) 239:332
Two crystal forms of the extracellular domain necrosis factor receptor.
a40737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stnfr1; type 1 receptor
#formal_name Homo sapiens #common_name man
expressed in Escherichia coli, residue 11 !
as a result of the expression system
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Crystal structure of the soluble human 55 kd TNF
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#disulfide_bonds
#length 160 #molecular-weight 18065 #checksum
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H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
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                                                                                                                         #length
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                                                                                                                                   *disulfide_bonds\
                                                                                                                                                                                                                                                                                                   protein; cytokine; signalling
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Pred. No. 5.83e-229;
1; Mismatches 0;
                                                          Score 1114; DB 5;
Pred. No. 5.14e-228;
1; Mismatches 0;
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                                                                                       Length 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crystallization and preliminary analysis tnf-beta-55 kd tnf receptor complex. Resolution: 2.85 angstroms Determination: X-ray diffraction Complex(lymphokineRECEPTOR)
                                                                                                                                                                                                                                                                                                                                                 55.4%;
Similarity 100.0%;
tumor necrosis factor receptor
contains residues 12 172 of t
chain A - hu
stnfr1; type i receptor
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D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, E.
Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.;
Lesslauer, W.
J. Mol. Biol. (1993) 229:555
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H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
Cell (1993) 73:431-445
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Pred. No. 6.85e-226;
0; Mismatches 0;
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                                kd extracellular mature receptor s
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Gentz,
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REFERENCE TN029039
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                         **residues 1-461 ##label ##cross-references GB:U19994; cession PC4093
                                                                                                                                                                                                                                                                                                        143
  ##molecule_type
##residues
                                                                     ##molecule_type mRNA
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Resolution: 2.25 angstroms
Determination: X-ray diffraction
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H.J.; Broger, C.; Loetscher, H.; Le
Cell (1993) 73:431-445
                                                                                                              Suter, B.; Pauli, U.
Gene (1995) 163:263-266
Cloning of the cDNA encoding
                                                                                                                                                                                    tumor necrosis factor receptor p55 - pigORGANISM 29-Nov-1995 *sequence_revision 08-reb-1996 *text_change 12-pec-1997
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J. Mol. Biol. (1994) 239:332
Two crystal forms of the extracellular domain
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expressed in Escherichia coli, residue 11 is mutated
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JC4302
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1-7 ##label SU2
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                                            PID:g1141753
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                                                                                 Query Match 42.2%;
Best Local Similarity 70.6%;
Matches 101; Conservative
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Matches
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##cross-references GB:M76656;
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SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
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Similarity 69.8%;
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#journal Mol. Immunol. (1993) 30:165-176
#title Genomic organization and promoter function of
tumor necrosis factor receptor beta gene.
#cross-references MUID:93156721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
KODTICNCHSGFFLRDKECVSCVNCKNADCKNLCPATSETRNDFQDTGTTVL 212
                                                                                                                                                                         13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; #superfamily tumor necrosis factor receptor type 1; NG receptor repeat homology cytokine receptor type 1; NG cytokine receptor #length 454 #molecular-weight 50030 #checksum 4267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology
glycoprotein; kidney; receptor; transmembrane protein; tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor necrosis factor receptor 02-Aug-1996 #sequence_revision 23-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothe, J.G.; Bluethmann, H.; Gentz,
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#domain NGF receptor repeat homology #label NG1\
#domain transmembrane #status predicted #label TMM\
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#product tumor necrosis factor receptor p55 #status
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                                                                                    Score 841; DB 2; L
Pred. No. 7.05e-164;
23; Mismatches 19;
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Pred. No. 3.26e-192;
22; Mismatches 26;
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NID:g202100;
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02-Aug-1996 #tes
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#journal
#title
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#title
                                                                                                                      #journal Immunogenetics (1994) 39:450-451
#title Nucleotide sequence of the TNF ty
endothelioma cell line.
*cross-references MJID:94245292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A. Mol. Cell. Biol. (1991) 11:3020-3026
#title Molecular cloning and expression of the type 1 and murine receptors for tumor necrosis factor.
#cross-references_MUID:91246168
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##residues 1.454 ##label RES
##cross-references GB:L26349; NID:g430732; PID:g430733
##This protein is one of two distantly related receptors
TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
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                                                                      **molecule_type mRNA
                                                                                                                                                                                                                                ##cross-references EMBL:X57796;
                                                                                                                                                                                                                                                              ##molecule_type mRNA
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Bur. J. Immunol. (1991) 21:1649-1656

Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834 Cloning and expression of cDNAs for two distinct murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES #formal_name Mus musculus #common_name house mouse 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                    S19021
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ss MUID:91187885
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Jenkins, N.A.; Smith,
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Smith, C.A.
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168-204
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236-454
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127-167
168-204
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#title
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#cross-references MUID:91090841 #accession B36555
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##cross-references GB:M63122; NID:g207361; PID:g207362
This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxin).

[FICATION #superfamily tumor necrosis factor receptor type 1; NGF
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##residues 1-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 DSYCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
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Similarity 70.6%;
101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
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#journal
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#journal J. Mol. Appl. Genet. (1981) 1:3-18

#title The gene encoding the common alpha
#cross-references MUID:82267643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #title Isolation, cloning and sequence analysis of the cDNA alpha-subunit of human chorionic gonadotropin. #cross-references_MUID:80011660
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Sairam,
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The amino acid sequences of the prepeptides contained in alpha and beta subunits of human choriogonadotropin.
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                                          restriction endonuclease evidence indicates that a single gene codes for the alpha chain common to the four dimeric hormones: thyrotropin, lutropin, follitropin, and choriogonadotropin previously the mature alpha chain (residues 25-116) was isolated from each of the hormones and its sequence was determined, as documented below
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#title Human pituitary thyrotropin.
alpha and beta subunits.
#cross-references MUID:77243687
#accession A90751
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Atlas,
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#authors Shome, B.; Parlow, A.F.

#journal J. Clin. Endocrinol. Metab. (1974) 39:199-202

#title Human follicle stimulating hormone (hFSH): first proposal:

the amino acid sequence of the alpha-subunit (hFSHalpha)

and first demonstration of its identity with the

alpha-subunit of human luteinizing hormone (hLHalpha).

#cross-references MUID:74262937

#contents annotation

anotation

A90632
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#journal J. Biol. Chem. (1975) 250:6735-6746
#title Primary amino acid sequence of follicle-stimulating hormone
from human pituitary glands.
#cross-references MUID:76005558
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Biochem. Biophys. Res. Commun. (1972) 48:530-537
Human pituitary interstitial cell stimulating hormone:
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J. Biol. Chem. (1975) 250:5247-5258
The amino acid sequence of human chorionic gonadotropin. The alpha subunit and beta subunit.
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Structure of human luteninizing hormone
Fujiki, Y.; Rathnam, P.; Saxena, B.B. Biochim. Biophys. Acta (1980) 624:428-4: Studies on the disulfide bonds in human
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human chorionic gonadotropin. the alpha subunit.
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#map_position 6914-6921
#introns 30/1; 91/3
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#journal Nippon Rinsho (1994) 52:940-947
#title [Structure and regulation of human thyroid-stimulating
hormone (TSH) gene].
#cross-references MUID:94254248
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##cross-references GB:S70585; NID:g546844;
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Local Similarity 93.5%;
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                            J. Biol. Chem. (1989) 264:6705
Preliminary x-ray diffraction analysis of human chorionic
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                                                                                                                  Nature (1994) 369:455
Crystal structure of human
                                                                                                                                                                                                                                    Lapthorn, A.J.; Harris, D.C.; Isaacs, N.W. submitted to the Brookhaven Protein Data Bank,
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Crystal structure of human chorionic gonadotropin.
annotation; X-ray crystallography, 3.0 angstroms; correction
of disulfide bonds
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              gonadotropin.
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experimental #label
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Pred. No. 1.71e-123;
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Best Local Similarity 98.8%; Pred. No. 1.99e-118;
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                                CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230
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Determination: theoretical model
complex; 91/coprotein hormone
phosphorylation; receptor
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Similarity 95.3%;
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Structure of human chorionic gonadotropin a from mad analysis of the selenomethionyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural predictions for the ligand-binding reglycoprotein hormone receptors and the nature hormone-receptor interactions structure.
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231 RVTVMGGFKVENHTGCHCSTCYY 253

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#cross-references PDB:1HCN 
REFERENCE TN020262
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ENTRY
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#authors
                                                                                                                                    KEYWORDS
                                   Query Match 27.6%;
Best Local Similarity 83.5%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.3%; Score 645; DB 5; Length 85; Best Local Similarity 98.8%; Pred. No. 1.99e-118; Matches 82; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6-56
24-78
28-80
55-83
                                                                                                                                                                                                                                              #authors Golos, T.G.; Durning, M.; Fisher, J.M.
#journal DNA Cell Biol. (1991) 10:367-380
#title Molecular cloning of the rhesus glycoprotein hormone
alpha-subunit gene.
#cross-references_MUID:91321740
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3-27
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                                                                                                         ##molecule_type DNA
##residues 1-120 ##label GOL
#FICATION #superfamily glycoprotein hormones alpha chain
RDS glycoprotein
RY #length 120 #molecular-weight 13785 #checksum
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                                                                                                                                                                                                              ##status
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35 CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CPECTIQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
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Resolution: 2.6 angstroms
Determination: X-ray diffraction
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Hendrickson, W.A.
Structure (1994) 2:545
Structure of human chorionic gonadotropin at 2.6 angstroms
resolution from mad analysis of the selenomethionyl
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Hendrickson, W.A.
submitted to the Brookhaven Protein Data Bank, July 1994
                                                                                                                                                                                                                              A39555
                                                                                                                                                                                                                                                                                                                                                                               glycoprotein hormones alpha chain precursor - rhesus mad
08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change
13-Jan-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A39555
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#disulfide_bonds\
#disulfide_bonds
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#region beta sheet\
#region beta sheet\
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                                 Score 551; DB 2; Length 120; Pred. No. 6.48e-97; 4; Mismatches 10; Indels
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Ol-MAY-1992 (REL. 22, LAST SEQU
Ol-WOV-1997 (REL. 35, LAST AND
TUMOR NECROSIS FACTOR RECEPTOR
TNFR1 OR TNFR-1.
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; V
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A., I
WONG G.H., CHEN E.Y., GOEDD
PROC. NATL. ACAD. SCI. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                       TNR1_MOUSE
P25118;
01-MAY-1992
01-MAY-1992
01-NOV-1997
                               SEQUENCE FROM N.A.

MEDLINE; 91285014.

BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P.,

GRAY P.W., FELDMANN M., FOXWELL B.M.J.;

EUR. J. IMMUNOL. 21:1649-1656(1991).
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CARBOHYD
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MEDLINE; 91246168.
MODDNIN R.G., ANDERSON D., JERZY R.,
COPELAND N.G., JENKINS N.A., SMITH C.
MOL. CELL. BIOL. 11:3020-3026(1991).
[3]
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 SEQUENCE FROM N.A
TISSUE-SPLEEN;
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llarity 69.8%;
Conservative
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GOEDDEL D.V.;
. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
RECEPTOR 1 PRECURSOR (P
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Pred. No. 3.
22; Mismatc
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POTENTIAL.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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.53e-226;
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                                                                                   KISSONERGHIS A.M.,
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   MEDLINE; 93156721.
MEDLINE; 93156721.
ROTHE J., BLUETHMANN H
MOL, IMMUNOL, 30.167
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-!- SUMILARITY: CONTA.
EMBL; M19468 (199826
EMBL; M59377; G202097
EMBL; X59238; G53579;
EMBL; X59738; G43073
EMBL; H76656; G202102
EMBL; M76656; G202102
EMBL; M76655; G202102
EMBL; M68067; G202102
EMBL; M68067; G202102
EMBL; M88067; G16677.
FIR; S19021; S19021
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ROTHE J., BLUETHAANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
ROL. IMMUNOL. 30:165-175(1993)
-i- FUNCTION: RECEPTOR FOR THE ALDHA. THE ADAPTOR MOLECULE FADD
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
PERFORMS CASPASE-8 PROTEDLYIC ACTIVATION WHICH INITIATES THE
SUBSEDUENT CASCALE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
SUBSEDUENT CASCALE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
PROTENSES) MEDIATING APOPTOSIS (BY SIMILARITY).
-i- SUBUNIT: TWE BINDING TO THE EXTRACELLUAR DOMAIN OF THER LEADS TO
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. INTERACTING
PROTEINS SUCH AS TRAFFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
TNER1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NF-KAPPA B SIGNALING (BY SIMILARITY).
-i- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; M5937; G202102; JOINED.
EMBL; M5937; G202102; JOINED.
EMBL; M76556; G202102; JOINED.
EMBL; M68067; G202102; JOINED.
EMBL; M76555; G202102; JOINED.
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PS50050; TNFR_NGFR_2;
PS50017; DEATH_DOMAIN;
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., LINTHICUM D.S.;
NETICS 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEMBRANE;
 TNFR1
 GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS
DEATH DOMAIN.
BY SIMILARITY
BOTENTIAL.
POTENTIAL.
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4 X TNER-CYS.
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TNER-CYS 2.
TNER-CYS 3.
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RA HIMLER A., MAURER-POGY I., KROENKE M., SCHEURICH P., PEIZENMAIER K.,
RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL DNA CELL BIOL. 9:705-715(1990).
CC -1- FUNCTION: RECEPTOR FOR TMR-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC RECRUITS CASPASE-8 PROTEDLYTIC ACTIVATION WHICH INTIATES THE
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION WHICH INTIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: TMF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. APOPTOSIS AND
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC 1- SUBGELULIAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC 1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CR EMBL: M63122: G207352: -
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Best Local :
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DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROMEDLINE; 910 HIMMLER A., LANTZ M., OL
                                                                                                                                                                                                                                                                                                  PROSITE; PSO0652; THFR_NGFR_1; 3.

PROSITE; PS50050; THFR_NGFR_2; 3.

PROSITE; PS50017; DEATH_DOMAIN; 1.

RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOR
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUR1_RAT STANDARD; PRT; 461 AA. P22934; PF22934; PF229345; PF22934; PF22934; PF22934; PF22934; PF22934; PF22934; PF229345; PF22934; PF22934; PF22934; PF22934; PF22934; PF22934; PF2293
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M63122; G207362;
PIR; B36555; B36555.
HSSP; P19438; ITNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TONTYCNCHAGEFLRESECVPCS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101;
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           4496614
7288614
7288614
72886614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50129
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      TNFR-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                          4 X TNFR-
TNFR-CYS
                                                                                                                      TNFR-CYS
                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                              EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                                                                                                     POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR 1.
                                                                                                                                                                                   X TNFR-CYS.
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                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Best Local S
Matches
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P01215;
21-JUL-1986 (REL. 01, C
21-JUL-1986 (REL. 01, L
01-NOV-1997 (REL. 35, L
GLYCOPROTEIN HORMONES A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID CARBOHYD
SEQUENCE OF 28-116.

MEDLINE; 72242988.

SAIRAM M.R., PAPKOFF H., LI C.H.;

BIOCHEM. BIOPHYS. RES. COMMUN. 48:530-537(1972).

[7]
                                                                                                                               SEQUENCE OF 28-116.
MEDLINE; 77243687.
SAIRAM M.R., LI C.H.;
CAN. J. BIOCHEM. 55:755-760(1977).
                                                                                                                                                                                                                                         SEQUENCE OF 1-24.

MEDLINE: 81117268.

BIRKEN S., FETHERSTON J., CANFIELD R.E.,

J. BIOL. CHEM. 256:1816-1823(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 80011660.
FIDDES J.C., GOODMAN H.M.;
NATURE 281:351-356(1979).
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-98 FROM N.A. MEDLINE; 82267643.
FIDDES J.C., GOODMAN H.M.; J. MOL. APPL. GENET. 1:3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 94254248.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIPPON RINSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIYOSHI I., KASAI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KONTVCTCHAGFFLRENECVSCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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98; Conser
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larity 68.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                  GOODMAN H.M.;
. GENET. 1:3-18(1981).
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52:940-947(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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50969
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)

ALPHA CHAIN PRECURSOR.
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Pred. No. 5.45e-18
21; Mismatches 1
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POTENTIAL.
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                                                                                                                                                                                                                                                                     BOIME
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AN:

AN ZUYLEN C.W.E.M., LEEFLANG B.R., HARD K., BOELENS R.,

KAMERLING J.P., VLIEGENTHART J.F.G.;

BIOCHEM. 241:229-242(1996).

JUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BEDLOGICAL SPECIFICITY TO THYROTROPIN,

LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

JR EMBL; JO0150; G183319; JOINED.

DR EMBL; JO0151; G183319; JOINED.

DR EMBL; S70585; G546845; JOINED.

DR EMBL; S70585; G546845; JOINED.

DR EMBL; V00485; G669156; JOINED.

PREMBL; V00485; G669156; JOINED.

PREMBL; V00487; G669156; JOINED.

PREMBL; V00487
 MEDLINE, SANCE RATHNAM P., SANCE STOL. CHEM. 7
             HORMONE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
MISE T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY ASSIGNMENT MEDLINE; 81006887.
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FUJIKI Y., RATHNAM P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BELLISARIO R., CARLSEN R.B., BAHL O.P., J. BIOL. CHEM. 248:6796-6809(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 25-116.
MEDLINE; 74011266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHOME B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE OF CARBOHYDRATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MORGAN F.J., BIRKEN S., CANFIELD R.E., J. BIOL. CHEM. 250:5247-5258(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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75211304.
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, PARLOW A.F.;
ENDOCRINOL. METAB.
                       PS00779; GLYCO_HORMONE_ALPHA_1; 1. PS00780; GLYCO_HORMONE_ALPHA_2; 1. GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAHL O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF 28-116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAXENA B.B.;
EM. 250:6735-6746(1975).
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624:428-435(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF DISULFIDE BONDS.
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GLYCOPROTEIN HORMONES ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BISHOP W.H.,
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                                                                                                                                                                                                                                                                                                      CHAIN
           231
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           RVTVMGGFKVENHTGCHCSTCYYHK
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Query Match
Best Local S
Matches
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Best Local S
Matches 7
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P22762;
01-AUG-1991 (REL. 1
01-AUG-1991 (REL. 1
01-OCT-1996 (REL. 2
                                                                                                                     DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                PROSITE;
PROSITE;
HORMONE;
SIGNAL
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                                                                                                                                                                                                                                                                                                                   MEDLINE;
GOLOS T.G
                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                         GOLOS T.G., DURNING M., FISHER J.M.;
DNA CELL BIOL. 10:367-380(1991).
-i-SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE
CHAIN WHICH CONTERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                    MACACA MULATTA (RHESUS EUKARYOTA; METAZOA; CH
                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           EUTHERIA;
                                                                                                                                                                                                                                                        A39555; A39555.
; P01215; 1HCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAKSYNRVTVMGGFKVENHTACHCSTCYYHKS
RVMVMGSVRVENHTECHCSTCYYHK 119
                           CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAKSYNRVTVMGGFKVENHTGCHCSTCYYHKS
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                                                                    Similarity 71; Conser
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                                                                                                                                                                                                                     PS00779; GLYCO_HORMONE_ALPHA_1; PS00780; GLYCO_HORMONE_ALPHA_2; GLYCOPROTEIN; SIGNAL.
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52
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83
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108
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(REL. 19, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
HORMONES ALPHA CHAIN PRECURSOR.
                                                                                                                                \frac{35}{60}
                                                                    Conservative
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93.5%;
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115
                                                                            27.6%;
83.5%;
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CHORDATA; VERTEBRATA; TETRAPODA;
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GLYCOPROTEIN HORMO
BY SIMILARITY.
                                                                   Score
Pred.
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CS -> SC (IN REF.
3BA19E2F CRC32;
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                                                                  re 551; DB 1; Le
d. No. 6.39e-114;
Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e 667; DB 1; Leu
1. No. 3.28e-145;
1. No. 5;
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21-JUL-1986 (REL. 01, C
23-OCT-1986 (REL. 02, L
01-NOV-1997 (REL. 35, L
GLYCOPROTEIN HORMONES A
GLYCOPROTEIN HORMONES A
GGA.
BOS TAURUS (BOVINE).
PROSITE;
PROSITE;
HORMONE;
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P01217;
21-JUL-1986
23-OCT-1986
01-NOV-1997
                                                                                                                                                                   -!- SUBUNIT: HETEROTIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH COMPERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, ECHAIN WHICH COMPERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, EUTROPIN, FOLLITROPIN AND GONADOTROPIN.

EMBL; X00003; E274391; -.

EMBL; X00004; E274391; JOINED.

EMBL; X00006; E607; -.

EMBL; X0005; G607; -.

PIR; A0143; TIBOA.

PIR; A05132; A05132.

HSSP; P01215; 1HCN.
                                                                                                                                                                                                                                                  CORNELL J.S., PIERCE J.G.;
J. BIOL. CHEM. 249:4166-4174(1974).
-1- SUBUNIT: HETERODIMER OF A COMMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE, 84041490.
GOODWIN R. 8., MOCHMAN C.L., ROTTMAN F.M.,
NUCLEIC ACIDS RES. 11:6873-6882(1983).
                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 80-91 AND MEDLINE; 72012932.
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 71
LIAO T.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 8-133 FROM N.A.
MEDLINE; 83161058.
NILSON J.H., THOMASON A.R., CSERBAK
J. BIOL. CHEM. 258:4679-4682(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 84024633.
                                                                                                                                                                                                                                                                                                          MAGHUIN-ROGISTER G., HENNEN G.P.;
EUR. J. BIOCHEM. 21:489-497(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERWIN C., CROYLE M.L., DONELSON
BIOCHEMISTRY 22:4856-4860(1983).
                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                        PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                       PIERCE
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 71111429
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-120.
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                                                                                                                                                                                                                                                                                                                                                                                                             BIOL.
                                                                                                                                                                                                                                                                                                                                                          ERCE J.G., LIAO T.-H., CARLSEN R.B.,
BIOL. CHEM. 246:866-872(1971).
                                                                                                                                                                                                                                                                                                                                                                                                           71111428.
H., PIERCE J.G.;
CHEM. 246:850-865(1971).
                                                                                                                                        PS00779; GLYCO_HORMONE_ALPHA_1; PS00780; GLYCO_HORMONE_ALPHA_2; GLYCOPROTEIN; SIGNAL.
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  13616
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
ALPHA CHAIN PRECURSOR.
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                                                                   GLYCOPROTEIN HORMONES A
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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O (IN REF. 4
A (IN REF. 1
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                 252
          REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.L.,
          <u></u>5
                                                                                                                    ALPHA CHAIN
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Best Local S
Matches 6
WEISCHAAR G., HIYAMA J., RENWICK A.G.C.;

LUR. J. BIOCHEM. 192:741-751(1990).

C -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNICHINAL CHAIN WHICH CONVERS BIOLOGICAL SPECIFICITY TO THYROTRO LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

REMBL; X16977; G1366; -.

R PIR; A01483; TTBOA.

R PIR; A01484; UTSHA.

R PIR; S06935; S06935.

R PIR; S06935; S06935.

R PIR; S06935; S06935.

R PIR; S06935; S0700, HORMONE_ALPHA_1; 1.

R PROSITE; PS00779; GLYCO_HORMONE_ALPHA_2; 1.

R PROSITE; PS00779; GLYCO_HORMONE_ALPHA_2; 1.

R PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.

R PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.

R POSITE; PS00780; GLYCO_HORMONE_ALPHA_1; 1.

R PROSITE; PS00780; GLYCO_HORMONE_ALPHA_1; 1.

R PROSITE; PS00780; GLYCO_HORMONE_ALPHA_1; 1.

R POSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.

R POSITE; PS00780; GLYCO_HORMONE_ALPHA_1; 1.

R POSITE; PS00780; SUBJECTER HORMONE_ALPHA_1; 1.

R POSITE; PS00780; SUBJECTER HORMONE_ALPHA_1; 1.

R POSITE; PS00780; SUBJECTER HORMONE_ALPHA_1; 1.

R POSITE; PS00780; SUBJECTER HORMON
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MEDLINE; 72211144.
LIU W.-K., NAHM H.S.,
WARD D.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLHA_SHEEP
P01218;
21-JUL-1986
01-APR-1990
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 90098887.
BELLO P.A., MOUNTFORD P.S., BRANDON M.R.,
NUCLEIC ACIDS RES. 17:10494-10494(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OVIS ARIES (SHEEP).
EUKARYOTA; METAZOA; CHC
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL 1986 (REL. 01, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS. CHUNG D., SAIRAM M.R., LI C.H.; ARCH. BIOCHEM. BIOPHYS. 159:678-682(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOCHEM. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAIRAM M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-120.
MEDLINE; 82113052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 73190034.
SAIRAM M.R., PAPKOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE OF CARBOHYDRATES
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Similarity 77.0%;
67; Conservative
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BIOPHYS. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWEENEY C.M., LAMKIN W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , LI C.H.;
153:554-571(1972).
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Pred. No. 4.06e-113;
7; Mismatches 13;
   GLYCOPROTEIN HORMONES ALPHA CHAIN. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.
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Best Local Similarity
Watches 67; Conserv
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P07474;
01-APR-1988
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SEQUENCE.

J. PROTEIN CHEM. 3:143-156(1984).

-1- SUBBURIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,

CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
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GLH1_RAT STANDARD; PRT; 120 AA. PL11962; P70516; 01-0CT-1989 (REL. 12, CREATED) 01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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HORMONE;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; LAGOMORPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
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                                                                                                                                                                              KAFTKATVMGNAKVENHTECHCSTCYYHKS 96
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D 14 64
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D 36 88
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larity 77.0%;
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LAST ANNOTATION UPDATE
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Pred. No. 4.06e-113;
7; Mismatches 13;
                                                                                                                                                                                                                                                                                                                           Score 546; DB 1; L. Pred. No. 1.39e-112;
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E -> Q (IN REF. 2).
E -> Q (IN REF. 2 TO
CS -> SC (IN REF. 3)
13BA4DE1 CRC32;
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Best Local S
Matches 6
                                                                                                              GLHA_BALAC STANDARD
P37035;
01-JUN-1994 (REL. 29, C
01-JUN-1994 (REL. 29, L
01-OCT 1996 (REL. 34, L
GLYCOPROTEIN HORMONES A
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RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                       BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-WISTAR-IMAMICHI;
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MEDLINE; 89196918.
BURNSIDE J., BUCKLAND
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GODINE J.E., CHIN W.W.,
SEQUENCE
                                  EUKARYOTA; METAZOA; CHORDATA; EUTHERIA; CETACEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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STRAIN-SPRAGUE-DAWLEY;
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L; V01252; G56580; -.

L; J00757; G206111; -.

L; M22829; -; NOT_ANNOTATED_CDS.

L; M25943; G204470; -.

L; M25544; G204471; -.

L; M25544; G204471; -.
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68; Conse
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I. 7:877-885(1990)
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S27385.
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257:8368-8371(1982).
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                                                                                                                                                                                                               STANDARD;
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78.2%;
                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
ALPHA CHAIN.
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AI T., KATO T.;
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T.,
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Pred. No. 4.78e-112;
6; Mismatches 13;
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; TETRAPODA; MAMMALIA;
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PROSITE;
HORMONE;
                                                                                                                                                                                                                                                                                     PROSITE;
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P11963;
01-OCT-1989 (REL. 12, CREATED)
01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
GLYCOPROTEIN HORMONES ALPHA CHAIN 2 PRECURSOR.
RATTUS NORVEGICUS (RAT).
RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KARASEV V.S., PANKOV Y.A.;
BIOKHTMIIA 50:1972-1986(1985).
-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
PIR; PN0138; PN0138.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                        PROSITE;
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GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF
                                                                                                                                                                                                                                                                                                                                                     $27386; $27386.
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                                                h 27.1%;
Similarity 77.0%;
67; Conservative
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61; Conser
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llarity 70.1%;
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                                              Score 541;
Pred. No. 3.
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Pred. No. 3.03e-111
13; Mismatches 13
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01-CCT-1996
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EMBL; J00643; G202180; -
EMBL; V00852; G54799; -.
EMBL; M22991; -; NOT_ANNOTATED_CDS.

EMBL; M22992; G575520; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 82060239.
CHIN W.W., KRONENBERG H.M., DI
PROC. NATL. ACAD. SCI. U.S.A.
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DNA 7:679-690(1988).
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                            170
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A31598; A31598.
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67; Conser
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Pred. No. 3.03e-111;
7; Mismatches 13;
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A. 78:5329-5333(1981).
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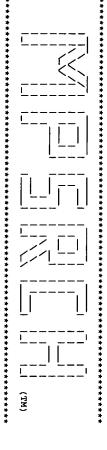
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ONES ALPHA CHAIN PRECURSOR.

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                 GLHA_STRCA STANDARD; PRT; 96 AA. P80665; 901-0CT-1996 (REL. 34, CREATED) 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) GLYCOPROTEIN HORMONES ALPHA CHAIN. STRUTHIO CAMELUS (OSTRICH). STRUTHIO CAMELUS (OSTRICH). STRUTHO CAMELUS (OSTRICH).
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HORMONE;
SIGNAL
CHAIN
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BIOCHEM. SOC. TEANS. 2:915-917(1974).
-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                                                          LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
EMBL; D00768; G217699; -.
EMBL; D00767; G217699; JOINED.
PIR; A01485; UTPGA.
PIR; A30339; A30339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 31-120.
MEDLINE; 74075725.
MAGHDIN-ROGISTER G., COMBARNOUS Y.,
EUR. J. BIOCHEM. 39:255-263(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KATO
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SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
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MEDLINE; 89325834.
HIRAI T., TAKIKAWA H.,
MOL. CELL. ENDOCRINOL.
          PALAEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                              Similarity 77.0%; 67; Conservative
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) (MAR-1992)
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77.08;
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) TO EMBL/GENBANK/DDBJ DATA BANKS.
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63:209-217(1989).
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Pred. No. 3.03e-111;
7; Mismatches 13;
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EUR. J. BIOCHEM. 240:262-267 (1996).
-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE
-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
MEDLINE; 97025333.
                                                                                                                                                                               SEQUENCE
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                                                                                       170
                                             230
                                                                 70
                                                                                                             10
                                                        TKITLKDNVKIENHTECHCSTCYYHKS
                                                                                                   GCPECKLGENRFFSKPGAPVYQCTGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKAF 69
                                             NRVTVMGGFKVENHTGCHCSTCYYHKS
                                                                                       GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229
                                                                                                                                   Similarity
65; Conse
                                                                                                                                                                                                                                                                      GLYCOPROTEIN
                                                                                                                                                                               96 AA;
                                                                                                                                                                                          11
32
33
56
56
82
                                                                                                                                   Conservative
                                                                                                                                              27.08;
74.78;
                                                                                                                                                                               10781 MW;
                                                                                                                                                                                            85988643
82645
            σ
            08:48:07 1998
                                                                                                                                 Score 538; Pred. No. 1.1
                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                               DDF7B4BB CRC32;
                                                                                                                                  e 538; DB 1; Le
. No. 1.92e-110;
Mismatches 12;
                                             256
                                                                 96
                                                                                                                                                                                                                                                                                  <u>. . . </u>
                                                                                                                                                        Length
                                                                                                                                     Indels
                                                                                                                                                         96;
                                                                                                                                   0;
                                                                                                                                   Gaps
                                                                                                                                   0,
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:47:32 1998; MasPar time 7.91 Seconds 811.687 Million cell updates/sec

Tabular output not generated.

>US-08-804-166-2 (1-256) from US08804166.pep 1994

Description: Perfect Score: Sequence: SRTSLLLAFGLLCLPWLQEG......GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150 Gap 11

Searched:

69112 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 42.029; Variance 63.165; scale 0.665

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

esult No:	Score	Query Match	Length	80	Ħ	Description	Pred. No.
_	1124	56.4	455	ٔ ب	TNR1_HUMAN	TUMOR NECROSIS FACTOR	3.58e-271
N	962		461	1		NECROSIS	٠. 3.5
ω	841		454	_	TNR1_MOUSE		8.77e-19
4	809	40.6	461	ب	TNR1_RAT	TUMOR NECROSIS FACTOR	5.45e-
, G	667	33.5	116	ب	GLHA_HUMAN	GLYCOPROTEIN HORMONES	3.28e-
σ	551	٠	120	Ь	GLHA_MACMU	GLYCOPROTEIN HORMONES	6.39e-
7	548	•	120	ш	GLHA_BOVIN	GLYCOPROTEIN HORMONES	4.06e-
- со	548		120	ᆫ	GLHA_SHEEP	GLYCOPROTEIN HORMONES	4.06e-
ω.	546	27.4	96	Н	GLHA_RABIT	GLYCOPROTEIN HORMONES	1.39e-
10	544	•	120	μ	GLH1_RAT	GLYCOPROTEIN HORMONES	4.78e-
11	541	27.1	96	μ	GLHA_BALAC	GLYCOPROTEIN HORMONES	3.03e-
12	541	27.1	120	Ľ	GLH2_RAT	GLYCOPROTEIN HORMONES	3.03e-
13	541	27.1	120	-	GLHA_MOUSE	GLYCOPROTEIN HORMONES	3.03e-
14	541	27.1	120	μ	GLHA_PIG	GLYCOPROTEIN HORMONES	3.03e-
15	538	27.0	96	_	GLHA_STRCA	GLYCOPROTEIN HORMONES	1.92e-110
16	539	27.0	120	۲	GLHA_CALJA	GLYCOPROTEIN HORMONES	1.04e-
17	537	26.9	120	_	GLHA_MELGA	GLYCOPROTEIN HORMONES	3.55e-110
18	535	26.8	96	μ	GLHA_PHYCA	GLYCOPROTEIN HORMONES	占
19	507	25.4	118	-د	GLH2_CYPCA	GLYCOPROTEIN HORMONES	3.54e-102
20	503	25.2	120	هــو	GLHA_EQUAS	GLYCOPROTEIN HORMONES	4.10e-101
21	501	25.1	96	۳	GLHA_HORSE	GLYCOPROTEIN HORMONES	1.39e-100
22	500	25.1	118	H	GLHA_HYPMO	GLYCOPROTEIN HORMONES	3 2.57e-100
23	500	25.1	118	1	GLH1_CYPCA	GLYCOPROTEIN HORMONES	2.57e-

4 4 5 4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
188 183	204	207	207	212	214	215	221	225	231	273	377	424	427	447	448	474	476	478	499	500
9.4 9.2	10.2	10.4	10.4	10.6	10.7	10.8	11.1	11.3	11.6	13.7	18.9	21.3	21.4	22.4	22.5	23.8	23.9	24.0	25.0	25.1
595 595	260	427	425	474	349	415	326	325	435	417	125	117	94	108	114	117	97	93	116	118
بر بر	-	Н	_	Н	_	Ь	Ь	Ь	ш	Н	μ.	щ	μ	μ	μ.	μ	_	ب	1	<b></b> -
FASA_BOVIN	CD27_HUMAN	NGFR_HUMAN	NGFR_RAT	TNR2_MOUSE	VC22_VARV	TNRC_MOUSE	VT2_MYXVL	VT2_SFVKA	TNRC_HUMAN	WSL1_HUMAN	GLHA_FUNHE	GLHA_ACALA	GLHA_THUOB	GLH1_ONCKE	GLH2_ONCKE	GLHA_ANGAN	GLHA_RANCA	GLHA_MURCI	GLHA_CLAGA	GLHA_CTEID
CD301 RECEPTOR PRECURS	CD27L RECEPTOR PRECURS	LOW-AFFINITY NERVE GRO	LOW-AFFINITY NERVE GRO	TUMOR NECROSIS FACTOR	PROTEIN C22/B28 HOMOLO	LYMPHOTOXIN-BETA RECEP	TUMOR NECROSIS FACTOR	TUMOR NECROSIS FACTOR	LYMPHOTOXIN-BETA RECEP	WSL-1 PROTEIN PRECURSO	GLYCOPROTEIN HORMONES									
1.52e-21 2.06e-20		6.44e-26	6.44e-26	4.37e-27	1.49e-27	8.65e-28	3.33e-29	3.76e-30	1.40e-31	8.97e-42	4.56e-68	2.80e-80	4.60e-81	2.62e-86	1.43e-86	1.99e-93	5.90e-94	1.74e-94	4.73e-100	2.57e-100

[6] SEQUENCE FROM N.A. MEDLINE; 92250049. FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS	RP SEQUENCE FROM N.A.  RP SEQUENCE FROM N.A.  RC TISSUE-PLACENTA;  RX MEDLLNE; 91017509.  RA GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN  RA GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN  RA PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).	SEQUENCE FROM N.A. MEDLINE; 91090841. HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURIC LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., DNA CELL BIOL. 9:705-715(1990).	UENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 LINE; 91066021. HAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., RKA D., HOLTMANN H., WALLACH D.; O J. 9:3269-3278(1990).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE; 90235284.  LOETSCHER H., PAN YC.E., LAHM HW., GENTZ R.,  TABUCHI H., LESSLAUER W.;  CELL 61:351-359(1990).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE-PLACENTA; MEDLINE; 90235285.  SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR CELL 61:361-370(1990).	JMAN). ZOA; CHORDATA; VERTEBRATA; TETRAPODA; IES.	P19438;  01-FEB-1991 (REL. 17, CREATED)  01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR BINDING PROTEIN 1) (THE) (PGO) (THE-RI) (PSO) (CT	RESULT 1 ID TUR1 HUMAN STANDARD: PRT: 455 AA.
AMBROS P.F.;	, FELDMAN M.; 990).	DRICH P., PEIZENMAIER K.,	10-124 AND 199-201. NN H., ZWANG R.,	R., BROCKHAUS M.,	ã	TRAPODA; MAMMALIA;	THOOR NECROSIS FACTOR	

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NETARPA B SIGNATING.

-I- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE

EMBL; X55313; G37244; -.

EMBL; M55266; G339745; -.

REMBL; M63121; G339756; -.

REMBL; M75866; G339750; -.

REMBL; M75866; G339750; JOINED.

REMBL; M75866; G339750; JOINED.

REMBL; M75866; G339750; JOINED.

REMBL; M75866; G339750; JOINED.

REMBL; M75865; G339750; JOINED.

REMBL; M75865; G339750; JOINED.

REMBL; M60275; G339750; JOINED.

REMBL; M60275; G339750; JOINED.

REMBL; A34899; G9HUT1.

R PIR; A34899; G9HUT1.

R PIR; A35010; A35010.

R PIR; A36208; A392057.

R PIR; A38208; A392057.

R PIR; A38208; A39206.
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                            TRANSMEM
DOMAIN
DOMAIN
REPEAT
                                                                                                                                                                              SIGNAL
CHAIN
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTION: RECEPTOR FOR THE ADAPTOR MOLECULE FADD
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH-INDICING SIGNALING COMPLEX (DISC)
PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
PROTEASES) MEDIATING APOPTOSIS.

-1- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THEFI LEADS TO
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
TNERI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
NET-YADDS B CITABLE TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NET-YADDS B CITABLE TO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
                                                                                        REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 97094982.

NAISMITH J.H., DEVINE T.Q., KHONO H., STRUCTURE 4.1251-1262(1996).

-I- FUNCTION: RECEPTOR FOR TNF-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BANNER D.W., D'ARCY A., CBROGER C., LOETSCHER H., CELL 73:431-445(1993).
                                                                                                                                                                                                                                                        PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGELMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 41-45
MEDLINE; 90110215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOMICS 13:219-224(1992).
[7]
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                                                                                                                                                                                                                                                                                                           1TNR; 31-JUL-94
1NCF; 07-DEC-95
1EXT; 11-JAN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N H., NOVICK D., WALLACH D
CHEM. 265:1531-1536(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93258809
                                                                                                                                                                                                                                              TRANSMEMBRANE;
D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LESSLAUER
                                                                                     TUMOR NECROSIS FACTOR RECEPTOR 1.

TUMOR NECROSIS FACTOR BINDING PROTEIN 1.

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 X THER-CYS.

TIMER-CYS. 1.

TIMER-CYS. 3.

TIMER-CYS. 4.

TIMER-CYS. 4.
                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPRANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.R.;
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SENTER B., PAULI U.H.;

RECEPTOR FOR THE ACTIVATED RECEPTOR MOLECULE FADD

C. --- FUNCTION: RECEPTOR FOR THE ACTIVATED RECEPTOR. THE RESULTING

C. --- FUNCTION: RECEPTOR FOR THE ACTIVATED RECEPTOR. THE RESULTING

C. RECRUITS CASPASE-8 TO THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

C. AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

C. AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX STREE

C. PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION WHICH INITIATES THE

C. SUBSEQUENT CASCADE OF CASPASES (ASPARTANTE-SPECIFIC CYSTEINE

C. PERFORMS CASCADE OF CASPASES (ASPARTANTE-SPECIFIC CYSTEINE

C. SUBSEQUENT CASCADE OF CASPASES (ASPARTANTE-SPECIFIC CYSTEINE

C. SUBSEQUENT CASCADE OF CASPASES (ASPARTANTE-SPECIFIC CYSTEINE

C. SUBURIT: THE SINDING TO THE EXTRACELLULAR COMAIN OF TNETAL THE LEADS TO

C. HONOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

C. PROVIDE A NOVEL MOLECULAR INTEFACE THAT INTERACTING

PROTITEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO

C. THER COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

C. NET VAPPA B SIGNALING (BY SIMILARITY).

C. INTERACTION: TYPE I NEMBRANE PROTEIN.

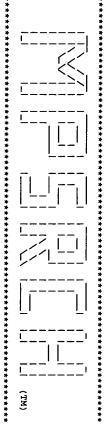
C. SUBCELLULAR LOCATION: TYPE I NEMBRANE PROTEIN.

PROSITE; PSO055; THER_NGFR_1; 3.

PROSITE; PSO055; THER_NGFR_1; 3.

PROSITE; PSO055; THER_NGFR_1; 3.

PROSITE; PSO055; THER_NGFR_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 14
RECEPTOR;
SIGNAL
CHAIN
DOMAIN
TRANSMEM
DOMAIN
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DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                     TNFR1.
SUS SCROFA (PIG).
SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNR1_PIG
P50555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (REL. 34, CARATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (INF-R1) (P55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 KONTVCTCHAGFFLRENECVSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                  TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455
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146
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168
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 461
210
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99.38;
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                                                                 GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS
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POTENTIAL.
POTENTIAL.
POTENTIAL.
MISSING (IN REF. 4).
GPAA -> APP (IN REF. 4)
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Pred. No. 3.58e-271;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
            POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:48:26 1998; MasPar time 13.91 Seconds 775.210 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-08-804-166-2 (1-256) from US08804166.pep 1994 1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150 Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent i1:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 41.143; Variance 64.343; scale 0.639

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Length	ВB	ID	Description	Pred. No.
فسو	945	47.4	180	4	Q95185	TUMOUR NECROSIS FACTOR	3.15e-213
ພ	895	44.9	471	4	019131	TUMOR NECROSIS FACTOR-	
ω	454	22.8	108	12	Q90287	GONADOTROPIN ALPHA SUB	σ
4	453		107	12	Q90286	GONADOTROPIN ALPHA SUB	
ر ت	451		119	12	Q91370	GONADOTROPHIN ALPHA 1	3.76e-84
σ	446	22.4	114	12	Q91371	GONADOTROPHIN ALPHA 2	6.95e-83
7	433		117	12	Q91119	GLYCOPROTEIN HORMONES	1.34e-79
œ	333	16.7	55	10	Q62589	ALPHA SUBUNIT OF GLYCO	1.06e-54
9	273	13.7	253	N	000276	LYMPHOCYTE ASSOCIATED	3.29e-40
10	273	13.7	380	N	000280	LYMPHOCYTE ASSOCIATED	3.29e-40
11	273	13.7	418	N	000275	LYMPHOCYTE ASSOCIATED	3.29e-40
12	257	12.9	277	N	014866	SOLUBLE DEATH RECEPTOR	2.00e-36
13	257	12.9	426	N	014865	DEATH RECEPTOR 3 BETA.	2.00e-36
14	214	10.7	348	11	Q85407	HOMOLOG OF VACCINIA VI	1.76e-26
15	214	10.7	349	11	089118	SOMALIA-1977 RIGHT NEA	1.76e-26
16	214	10.7	349	11	860680	GARCIA-1966 RIGHT NEAR	
17	210	10.5	355	11	Q85308	SECRETED RECEPTOR BIND	1.42e-25
18	206	10.3	459	10	Q62327	TUMOR NECROSIS FACTOR	1.13e-24
19	187	9.4	267	4	002764	OX40 PRECURSOR (FRAGME	<u>-</u>
20	182	9.1	259	N	014755	TRAIL RECEPTOR 3.	2.34e-19

4 4 4 0	43	42	41	40	39	38	37	36	ω 5	34	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21
146 143	148	147	150	152	153	153	154	156	155	160	160	161	167	167	174	174	174	174	174	178	179	180	180
7.3 7.2	7.4		7.5		7.7	7.7	7.7		7.8	•	8.0		8.4	8.4	8.7	8.7	8.7	8.7		8.9		٠	9.0
217 212	401	217	274	401	625	401	199	372	217	245	202	468	217	202	440	440	411	411	411	324	425	299	283
44	10	4	N	10	10	N	N	N	N	N	N	N	N	N	N	N	N	N	N	10	N	N	2
Q07369 Q07368	008727	Q07367	Q13663	008712	035305	000300	Q14406	000279	Q14407	014644	014643	000220	Q16631	Q14405	014763	015531	014720	015517	015508	Q63199	Q16042	014798	Q92956
SOMATOTROPIN 3 PRECURS SOMATOTROPIN 2 PRECURS	RIN		CELL SURFACE ANTIGEN O	OSTEOPROTEGERIN.	RANK.	OSTEOPROTEGERIN.	CHORIONIC SOMATOMAMMOT	LYMPHOCYTE ASSOCIATED	CHORIONIC SOMATOMAMMOT	PLACENTAL GROWTH HORMO	PLACENTAL GROWTH HORMO	CYTOTOXIC LIGAND TRAIL	SOMATOTROPIN PRECURSOR	SOMATOTROPIN PRECURSOR	APOPTOSIS INDUCING REC	APOPTOSIS INDUCING PRO	DEATH RECEPTOR 5.	CYTOTOXIC TRAIL RECEPT	P53-REGULATED DNA DAMA	FAS ANTIGEN PRECURSOR.	TUMOR NECROSIS FACTOR	CYTOTOXIC TRAIL RECEPT	HERPESVIRUS ENTRY MEDI
	3.68e-12		1.43e-12	5.55e-13	3.45e-13	•	2.14e-1	8.23e-14	1.33e-13		1.20e-14	7.40e-15	3.98e-1	3.98e-1	1.27e-17	1.27e-17	1.27e-17	1.27e-17	1.27e-1	1.73e-1	1.05e-1	6.38e-1	6.38e-

Dr AC	RESULT	Оу	Оу	Оy	Qu Be Ma	RP RA RP DR CORRESPONDENCE OF THE CORRESPOND		RESULT ID Q
019131; 01-JAN-1998 (TREMBLREL. 05, CREATED)	LT 2. O19131 PRELIMINARY; PRT; 471 AA.	165 TVCTCHAGFFLRGNEC 180	105 KCRKEMYQVBISPCTVYRDTVCGCRKNQYRYYWSETHFQCLNCSLCLNGTVQISCKETQN 164 	45 CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104	Query Match 47.4%; Score 945; DB 4; Length 180; Best Local Similarity 86.0%; Pred. No. 3.15e-213; Matches 117; Conservative 9; Mismatches 10; Indels 0; Gaps 0	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  DUTHIE S., NASIR L., ECKERSALL P.D.;  DUTHIE S., NASIR L., ECKERSALL P.D.;  SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.  EMBL; U72344; G1613880;  PROSITE; PS00652; TMFR_NGFR_1; 3.  NON_TER 1 1 1  NON_TER 1 1 1  NON_TER 180 180  SEQUENCE 180 AA; 20399 MW; 5452A6B2 CRC32;	Q95185; Q1-FEB-1997 (TREMBLREL. 02, CREATED) Q1-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE) Q1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT). TNFR-1. FELIS SILVESTRIS CATUS (CAT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; CARNIVORA.	JT 1 Q95185 PRELIMINARY; PRT; 180 AA.

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RESULT
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Best Local 9
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Best Local
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES;
EUKARYOTA; METAZOA; CHORDATA; CYPRINIFORMES.
  Q90286;
01-NOV-1996
01-NOV-1996
01-NOV-1996
                                                            Q90286
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NON_TER
SEQUENCE
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Q90287
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SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; D86552; G1469838; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEE E.-K., TALYOR M.J., KEHRLI M.E.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; U90937; G2290398; -
PROSITE; PS00652; TMFR_NGFR_1; 3.
SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF-RI.
BOS TAUTOS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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01-JAN-1998
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                                                                                                                                  88
                                                                                                                                                                                                     Match 22.8%;
Local Similarity 72.0%;
les 59; Conservative
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                                                                                                                           KRVLV-DDVKLVNHTDCHCSTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KONTVCTCHAGFFLRENECVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160
                                                                                                          NRVTVMGGFKVENHTGCHCSTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RODTICHCHMGFFLKGAKCISC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
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Similarity 73.2%;
104; Conservative
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108 AA;
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(TREMBLREL.
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                                                            PRELIMINARY;
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12129 MW;
 9,9,9
CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                     Score 454; DB 12; 1
Pred. No. 6.53e-85;
7; Mismatches 15;
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                                                                                                          251
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                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Q1-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
GONADOTROPHIN ALPHA 1 SUBUNIT.
ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91371;
01.NOV-1996 (TREMBLREL. 01, CREATED)
01.NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01.JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01.JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
0CONADOTROPHIN ALPHA 2 SUBUNIT.
0CONADOTROPHIN ALPHA 2 SUBUNIT.
0CONADOTROPHIN METAZOA; CHORDATA; VERTEBRATA; PISCES; G
0STEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
                                                                                                                                                                                                                                                                       LT 6
Q91371
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SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; D86551; G1469836; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAAOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 94197892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 GCPECTIQENPETSQPGAPILQCMGCCFSRAYPTPLRSKTMLVQKNVTSESTCCVAKSY 229
                                                                                                                                                                                                                                                                                                                                                                           230
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                                                                                                                                                                                                                                                                                                                                                                   34 GCEECKLKENKLFSNPGAPVYQCTGCCFSRAYPTPLQSKKAMLVPKNITSEATCCVAKEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRVTVMGGFKVENHTGCHCSTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.6%;
Similarity 67.8%;
59; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n 22.7%;
Similarity 72.0%;
59; Conservative
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107 AA;
                                                                                                                                                                                                                                                                       PRELIMINARY;
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Pred. No. 3.76e-84;
11; Mismatches 16;
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Pred. No. 1.17e-84;
7; Mismatches 15
                                                                                                                                                                                                                                                                       PRT;
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                                                                     GNATHOSTOMATA;
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RESULT 7
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Best Local
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Best Local :
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                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91119;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. MOL. ENDOCRINOL. 11:265-273(1593).

J. MOL. ENDOCRINOL. 11:265-273(1593).

EMBL; S69274; G546260; -.

EMBL; S69274; G546260; -.

PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.

PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.

PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
                                                                                                                                       DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN) (GTH-ALPHA).

MORONE SAXATILIS (STRIPED BASS)

EUKARYOTA, METAZOA; CHORDATA; VI

OSTEICHTHYES; ACTINOPTERYGII; P.
                                                                                                                                                                                                                                                                                                                                                                              TISSUE-PITUITARY G
MEDLINE; 96020549.
HASSIN S., ELIZUR
                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                     SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOPROTEIN HORMONES ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 94197892.
GEN K., MARUYAMA O.,
                                                                                                                                                                                                                                                                                                                             HASSIN S
                                                                                                                                                                                                                                                                                                                                      TISSUE-PITUITARY GLAND;
                                                                                                                              SEQUENCE
                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                        HORMONE;
                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170
                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
 229
                                          170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 GCEECTLKPNTIF--PN--IIQCTGCCFSRAYPTPLRSKQTMLVPKNITSEATCCVAKEG
                     92
                                                              33
                                                                                             Local
                                                                                                                                                                                                                                                                        SIMILARITY).
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA
L; L35071; G2322657; -.
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                                        GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229
YNRVTVMGGFKVENHTGCHCSTCYYHK
            YE-TEV-AGIKVRNHTDCHCSTCYFHK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRVTVMGGFKVENHTGCHCSTCYYHKS
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62; Conser
                                                                                                                                                                                                                                                                                                                                                                    ENDOCRINOL.
                                                                                  Similarity
57; Conser
                                                                                                                                                                                                                                               PS00779; GLYCO_HORMONE_ALPHA_1; PS00780; GLYCO_HORMONE_ALPHA_2;
                                                                                                                                                                                                                                        GLYCOPROTEI
                                                                                                                                                                                                                                                                                                                                                           ELIZUR A., ZOHAN ...
TOTRINOL. 15:23-35(1995).
                                                                                                                            1
24
34
37
54
58
58
58
78
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
N HORMONES ALPHA CHAIN PRECURSOR (GONADOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    GLAND;
                                                                                             21.7%;
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71.38;
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57
86
107
109
112
78
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11:265-273(1993).
                                                                                                                              13066 MW;
                                                                                                                                                                                                                                        SIGNAL.
                                                                                                                                               BY SIMILARITY.
GLYCOPROTEIN HORMONES A
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 446; DB 12;
Pred. No. 6.95e-83;
6; Mismatches 15
                                                                                 Score 433; DB 12; I
Pred. No. 1.34e-79;
14; Mismatches 12;
                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   PERCIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              VERTEBRATA;
                                                                                                                             CAFB9D0C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                              PISCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAKABAYASHI
                                                                                                                                                                                                                                                                                CHAIN (BY
                                                                                                       Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GNATHOSTOMATA,
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                                                                                  Indels
                                                                                                                                                                                                                  ALPHA CHAIN
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Best Local S
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Matches
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01-JUL-1997 (TREMBLREL. 04, LAST
01-JAN-1998 (TREMBLREL. 05, LAST
101-JAN-1998 (TREMBLREL. 05, LAST
LYMPHOCYTE ASSOCIATED RECEPTOR 01
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
ALPHA SUBUNIT OF ELYCOPROTEIN HORMONES (FRAGMENT).
PHODOPUS SUNGORUS (STRIPED HAIRY-FOOTED HAMSTER) (DJU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 8
Q62589
                                                                                                                                                                                                            PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              LT 9
000276
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                  SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ EMBL; U94503; G2071953; -.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. SCREATON G., XU X.N.,
                                                                                                                                                                                                                                                                                                                                                                                          000276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOCKMANN J., BOCKERS T.M., VENNEMANN WITTKOWSKI W., SABEL B., KREUTZ M.R.; ENDOCRINOLOGY 137:1804-1813(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-PITUITARY;
MEDLINE; 96198779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        EUTHERIA; PRIMATES.
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                             202
                                             129
                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                          69
                                                                                                                                      13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS
                                                                                                                                                                         Local
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PERCA 192
                                                                 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S
                                   TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT
                       ENLFQC-FNCSLCLN-GTVH---
                                                                                         TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X90776; E195654;
                                                                                                                                                              Similarity 60; Conser
                                                                                                                                                                                                            PS00652;
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                                                                                                                                                             13.7%;
larity 32.4%;
Conservative
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                                                                                                                                                                                                            TNFR_NGFR_1;
; 26934 MW;
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                                                                                                                                                                                                                                                                                                                    CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                    OLSEN A., COWPER A., TAN R., MCMICHAEL
                                                                                                                                                                                                                                                                                                                                         04, CREATED)
04, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
ECEPTOR OF DEATH 2.
                                                                                                                                                             Score 273; DB 2; L4
Pred. No. 3.29e-40;
34; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 333; DB 10;
Pred. No. 1.06e-54;
6; Mismatches 7
                       -LSCQEKONTVC-TCHAGFFLRENECVSCAGAAPG-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E5AAE0F8
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                                                                                                                                                                                                         2.
A21C863E CRC32;
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                                                                                                                                                                                                                                             DATA BANKS
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                                                                                                                                                              Indels
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                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             256
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ID O
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Best Local S
Matches 6
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000275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDAT
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O00280
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; U94510; G2071967; -. PROSITE; PS00652; TMER_NGFR_1; 2. SEQUENCE 380 AA; 41192 MW; 17C92A14 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SCREATON G., XU X.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  000275;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  000280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                             y Match 13.7%;
Local Similarity 32.4%;
les 60; Conservative
               52
                                                                                       69
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nes 60; Conser
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DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119
                                                                                                                                              TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61
                                                                                                                                                                                                                             AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS
                                                                       TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PE-CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 273; DB 2; larity 32.4%; Pred. No. 3.29e-40; Conservative 34; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLSEN A., COWPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLSEN A., COWPER A., TAN
                                                                                                                                                                                                                                                                                                 Score 273; DB 2; Length 418;
Pred. No. 3.29e-40;
34; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BANKS
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                                                                                                                                                                                                                                                                                                         Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCMICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAMMALIA;
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                         13;
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ID 014866
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           Query Match
Best Local S
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Best Local :
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                  SALLES G.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ
SUBMIT AF026070; G2570831; -.
PROSITE; PS00652; TNFR_NGFR_1; 2.
SEQUENCE 426 AA; 45950 MW; 87E00821 CF
                                                                                                                                                                                            O14865;
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O14866;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; AF026071; G2570833; -. PROSITE; PS00652; TMPR_MGFR_1; 2. SEQUENCE 277 AA; 29111 MW; 06E165C7 CRC32;
                                                                                                   WARZOCHA K.,
                                                                                                                                                                                    DEATH RECEPTOR 3
                                                                                                                                                                                                                                                       014865
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SALLES G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOLUBLE DEATH RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WARZOCHA
                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                                                                 120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG
                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                      62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119
                                                                                                                                                                                                                                                                                                                                                                                        3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61
                                                                                                                                                                                                                                                                                                                                                                  TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PE-CT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERCA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG-C 171
        n 12.9%;
Similarity 31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     h 12.9%;
Similarity 31.5%;
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K., RIBEIRO P.,
                                                                                                    RIBEIRO P.,
  Conservative
                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                    BETA.
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                                                                                                                                                                                          05, CREATED)
05, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
                                                                                                    RENARD N., CHARLOT C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RENARD N.,
Score 257; DB 2; Le
Pred. No. 2.00e-36;
34; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 257; DB 2;
Pred. No. 2.00e-36;
34; Mismatches 73
                                                                                                                                                VERTEBRATA;
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARLOT
                                                                                                                                                                                                                                                     426
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                                             CRC32;
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                                                                              DATA
                                                                                                                                                  TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         С.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                      Length 426;
                                                                              BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BANKS
                                                                                                    COIFFIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COIFFIER
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Indels
15;
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Gaps
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11;
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69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128

13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS

TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT

61 8

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SOR RACE OCCUPANT OCC
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ID Q85407
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Best Local Similarity 38.5%;
Matches 30; Conservative
    Query Match 10.7%;
Best Local Similarity 38.5%;
Matches 30; Conservative
                                                                                  SEQUENCE FROM N.A.

STRAIN-SOMALIA-1977;

WASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E.,
TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;

SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; U18341; G885855; -.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00652; TNFR_NGFR_1; 2.

TOTTENCE 349 AA; 38272 MW; OFDCC784 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q85407;
01-NOY-1996 (TREMBLREL. 01, CREATED)
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
HOMOLOG OF VACCINIA VIRUS CDS B28R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q89118;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
SOMALIA-1977 RIGHT NEAR-TERMINAL REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 15
Q89118
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MEDLINE; 94080747.

MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,

KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;

NATURE 366:748-751(1993).

EMBL; L22579; G439102; -

PROSITE; PS00652; TMFR_MGFR_1; 2.

SEQUENCE 348 AA; 38075 MW; 2A911AF6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIOLA VIRUS.
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
ORTHOPOXVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIOLA VIRUS.
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORTHOPOXVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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14; Mismatches 32;
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14; Mismatches 32;
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Search completed: Wed Job time: 78 secs. Мау 6 08:49:44 1998

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:57:57 1998; MasPar time 1227.99 Seconds 1496.959 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-804-166-3 (1-1202) from US08804166.seq 1202

1 CTCGAGATGGCTACAGGTAA.......CCCCGATCCTCCCACAATAA 1202 GAGCTCTACCGATGTCCATT.......GGGGCTAGGAGGGTGTTATT

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

436399 segs, 764661465 bases x 2

Database:

emb153
1:em\_in 2:em\_or 3:em\_om 4:em\_ov 5:em\_pl 6:em\_htg
1:em\_hum1 8:em\_hum2 9:em\_ba 10:em\_ro 11:em\_un 12:em\_vi
13:em\_pat
genbank105
14:gb\_ro 15:gb\_om 16:gb\_ov 17:gb\_in 18:gb\_pl 19:gb\_ba
20:gb\_st 21:gb\_vi 22:gb\_ph 23:gb\_sy 24:gb\_un 25:gb\_pat
26:gb\_htg 27:gb\_pr1 28:gb\_pr2

Database:

Statistics: Mean 11.143; Variance 5.206; scale 2.140

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query Match	Query Match Length	DB	ID	Description	Pred. No.	
<b>_</b>	424	35.3	483	25	A29099	Synthetic DNA for TNF-	0.00e+00	
N	424	35.3	510	25	A21525	oligonucleotide probe.	0.00e+00	
ω	424	35. 3	600	25	A20257	Synthetic nucleotide s	0.00e+00	
4	424	35.3	1331	25	A29103	H.sapiens mRNA for TNF	0.00e+00	
U	424	35.3	1368	25	A29098		0.00e+00	
σ	424	35.3	2050	27	HUMTNFRP	Human tumor necrosis f	0.00e+00	
7	424	35.3	2062	25	I43805	Sequence 24 from paten	0.00e+00	
8	424	35.3	2062	25	A21522	TNF alpha gene.	0.00e+00	
9	424	35.3	2087	27	HUMTNER	Human tumor necrosis f	0.00e+00	
10	424	35.3	2111	27	HUMINFRB	Homo sapiens tumor nec	0.00e+00	
11	424	35.3	2111	25	A26412	cDNA for (55kD INF-BP)	0.00e+00	
12	424	35.3	2112	27	HUMTNFRC	Human tumor necrosis f	0.00e+00	
13	424	35.3	2161	27	HSTNFR1A	H.sapiens TNF-R mRNA f	0.00e+00	
14	424	35.3	2175	25	A43873	Sequence 1 from Patent	0.00e+00	

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H.sapiens mRNA for TNF-binding A29103
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Location/Qualifiers
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Hom
1 (bases 1 to 1331)
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Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stra
TNF-receptor, TNF-binding protein and DNA coding
Patent: EP 0393438-A 48 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
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                                                                                                  Draft entry and computer-readable sequence for [Proc. Sci. U.S.A. (1990) In press] kindly submitted by P.W.Gray, 13-AUG-1990.
                                                                                                                                                   Gray, P.W., Barrett, K.J., Chantry, D., Turner, M. and Feldman, Cloning of human tumor necrosis factor (TNF) receptor cDNA expression of recombinant soluble TWP-binding protein Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordat
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2050)
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larity 99.8%;
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                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
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/db_xref="taxon:29278"
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/gene="TNF
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Pred. No. 0.00e+00;
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I43805
                                     1 (bases 1 to 2062)
Feldmann, M., Gray, P.W., Turner, M.J.C. and Brennan, F.M.
TNF. alpha. receptor-derived binding protein
Patent: US 5633145-A 24 27 MAY-1997;
                                                                                                                                                g2468903
                                                                                            Unclassified
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/product="TNF receptor"
/product="TNF receptor"
/db_xref="FDD: 93.9760"
/translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
PGKY IHPQNNSICCTKCHKGTYLYNDCPGPGDDTDCRECESGSFTASSNHLRIGLSC
SKCRKEMGOVELSSCTVDRDTVCGCRKNOYRHWSENLFQCFNCSLCLNGTYLLRICLSC
SKCRKEMGOVELSSCTVDRDTVCGCRKNOYRHWSENLFQCFNCSLCLNGTYVLLPLVI
EFGLCLLSLLFIGLMYRYGRMKSKLYSIVCGKSTPERSGELEGTTTKPLAPNSFSPT
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            Location/Qualifiers
1. .2062
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275. .1513
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PNPLOKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
/organism-"unknown'
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A21522
g579599
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
l (bases 1 to 2082)
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425; Conser
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ffglcllslifiglmyrygnksklysivcgkstperegelegttrlatalasspf
pgftptigfsgvpsgstftsssfytpgcpnfaaprreyappyrdlglsdheidrleiqn
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                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
155. .1522
                                                                                                                                                               /gene="TNF alpha gene"
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Best Local Similarity 99.8%;
Matches 425; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2087)
Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., Won Gatanaga, T., Granger, G.A., Lentz, R., Raab, H., Kohr, W.J. and Goeddel, D.V.
                                                                                                                                                                                                                                                                                  Draft
by T.s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell surface receptor; tumor necrosis factor receptor. Human placenta, cDNA to \mathtt{mRNA}.
                                                                                                                                                                                                                                                                                                                                                       necrosis factor
Cell 61, 361-370 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tumor
                                                                                                                                                                                                                                                                                                                                                                                                               Molecular cloning and expression of a receptor for human tumor
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                                                                                                                                                                                                                                                                                    entry and computer-readable sequence schall, 26-MAR-1990.
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/codon_start=1
/codon_start=1
/rodon_start=1
/rodon
                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
182. .1549
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                                                                                                                                                                                                                                    Location/Qualifiers
1. .2087
                                                                                                                                  /note="tumor necrosis factor receptor"
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                                                                                                                                                                                                                                                                                                            for [1] kindly submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice,G.C., Wong,G.H.,
Kohr,W.J. and
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FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNPAAPRREVAPPYQGADPILATALASDPI
PNPLQWEDSAHKPGSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
GRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
PSLLR"
433 a 624 c 581 g 449 t
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•	TIT JOU MED FEATU	DEFINITI ACCESSIO NID KEYWORDS SOURCE ORGANI REFERENC AUTHOR	RESULT LOCUS	Оy	ОУ	ОУ	oy B	oy Db	Qy Db	δλ B	g pb	Que Bes Mat
sig_pe	LE RNAL LINE RES SOURC	DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	ш	722 1	705 1	645	542 (	482 <i>l</i> 525 <i>l</i>	422 1	362 <i>l</i>	302 (	Query Match Best Local S Matches 42
b_xref="taxon:98 11.1ne="HL60" 7273 7273 ene="TNF receptoroduct="tumor neceptoroduct="tumor neceptoroduct="t	Molecular cloning and exp factor receptor Cell 61, 351-359 (1990) 90235284 Location/Qualifi e /organism="Homo	Homo sapiens tumor necrosi M58286 M33480 g339753 tumor necrosis factor rece Human cell line HL60, cDNA Homo sapiens Eukaryotae; mitochondrial Vertebrata; Eutheria; Prim 1 (bases 1 to 2111) Loetscher, H., Pan, YC.E., Tabuchi, H. and Lesslauer, W	10 HUMTNFRB 2111 bp mRNA PRI 14-NOV-1990	TCCTGT 727	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTC	TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 661	CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 601 	AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 541	TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 481 	AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 421 	GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 361 	tch 35.3%; Score 424; DB 27; Length 2087; al Similarity 99.8%; Pred. No. 0.00e+00; 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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KEYWORDS
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Matches 425;
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1 (bases 1 to 2111)
Brockhaus, M., Dembic, Z.,
Schlaeger, E.J.
                                                                                                                                                                                                                                       patent EP0417563.
A26412
                                                                                                                     unidentified
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                                                                                                                                                                                                                                                                                              cDNA for (55kD TNF-BP)
                                                                                       unclassified.
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larity 99.8%;
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/gene="TNF
274. .1551
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/note="55 kDa"
/codon_start=1
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Pred. No. 0.00e+00;
0; Mismatches 1
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                              Gentz, R.,
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                              Lesslauer, W.,
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                              Loetscher, H.
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Best Local :
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g339755
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H l (bases 1 to 2112)
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425; Conser
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Patent: EP 0417563-A 24 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
                                                                      Human cDNA to mRNA.
                                                                                                                                                           Human tumor necrosis
                                                     Homo sapiens
                                                                                        tumor necrosis factor
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llarity 99.8%;
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//translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC/
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KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
FFGLCLLSLLFIGLMYRKQRWSSLYSIVCGKSFLEKGSLESCTTTK PLAPNPSFSPT
GFFTFIGFSVPPSSTTYSSTYTFGDCPNFAAAPRREVAPFYQGADFILATALASDFI
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GRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
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187. .1554
Inote="pid:e161624"
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Best Local Similarity 99.8%;
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Molecular cloning and expression
factor receptor chain (p60) and i
necrosis factor-binding protein
DNA Cell Biol. 9, 705-715 (1990)
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/db_xref="pin:9339756"
/db_xref="pin:9339756"
/tanslation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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FFGLCLLSLEJGLAWRYQRWKSKLVSIVCGKSTPEKEGELEGTTTRFLAPNPSFSPT
PGFTPILGFSPVPSSTFTSSSTTTPGDCPNFAAPRRVAPPYGGADFILATALASDPI
PRILGWEDSAHKPGSLDTDDPATLYAVVENVPLKWKEFVRRLGLSDHEIDRLELON
PNPLJGWEDSAHKPGSLDTDDPATLYAVVENVPLKWKEFVRRLGLSDHEIDRLELON
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/db_xref="taxon:9606"
207. .293
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/product="tumor necrosis factor
632 c 589 g 456 t
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Best Local Similarity 99.8%;
Matches 425; Conservative
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 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                         AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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/note="putative"
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757. .857
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/rodouct="tunor necrosis factor receptor type 1"
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PRIJGWEDSAHKPGSLDTDDPATLYAVVENVPPLRWKETVRRLGSDHEIDBLELQN
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2145. .2150
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                                                                                                     GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTGCTGTACC 435
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AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
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Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
Proteases capable of shedding the soluble TNF-receptor and TNF-R
derived peptides and antibodies against the proteases inhibiting
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PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKBFVRRLGLSDHEIDRLBLQN
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                                                                                         AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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Wallach,D., Brakebusch,C., Varfolomeev,E.
Molecules influencing the shedding of the
preparation and their use
Patent: US 5665859-A 1 09-SEP-1997;
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MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 13:37:52 1998; MasPar time 155.56 Seconds 891.677 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence: Title: >US-08-804-166-3 (1-1202) from US08804166.seq 1202

Comp: 

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.195; Variance 5.326; scale 1.727

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query Match	Length	BU	Ħ	Description	Pred. No.
1	424	35.3	808	4	Q24441	Encodes truncated TNF	1.67e-282
N	424	35.3	1334	۳	Q06282	Plasmid Tumour Necros	1.67e-282
ω	424	35.3	1368	œ	Q49932	Lambda-derived TNF-R	1.67e-282
4	424	35.3	2062	4	Q24440	Encodes TNF-alpha 55k	1.67e-282
υ	424	35.3	2062	ω	Q20973	TNF-alpha binding pro	1.67e-282
σ	424	35.3	2088	N	Q10883		1.67e-282
7	424	35.3	2111	N	Q10955	Encodes human 55kD TN	1.67e-282
œ	424	35.3	2141	μ.	Q06285	Human Tumour Necrosis	1.67e-282
9	424	35.3	2175	15	Q90513	p55 TNF-R gene.	1.67e-282
10	424	35.3	6889	18	T15931	DHFR/intron (WTrasSD)	1.67e-282
11	422	35.1	2170	ø	Q50870	p55 Tumour necrosis f	4.91e-281
12	422	35.1	2176	N	Q12215	Type I TNF receptor.	4.91e-281
13	414	34.4	579	ω	Q14800	Human chorionic gonad	3.68e-275
14	409	34.0	836	17	T03212	Single chain gonadotr	1.73e-271
15	409	34.0	836	17	T03243	Single chain gonadotr	1.73e-271

밁

129 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 188

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4444 5443 5443	4333334 400887654	3333098876584332109887768
77 72 71 71	184 179 169 130 101 99	3815 315 300 300 300 300 200 276 276 276 276 276 276 276 276 276 276
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Human Natriuretic Pep DNA encoding hCG beta Sequence encoding hum Sequence encoding pre Human pro-growth horm	LH sub LH sub ncated uence o coding to 41 f	Encodes truncated TNF Single chain gonadotr Rat Fabpl gut-specifi Encodes truncated TNF Human growth hormone Human growth hormone Sequence encoding hum Single chain gonadotr Single chain tonated TNF Encodes truncated TNF Bovine beta LH subuni Porcine beta LH subuni Sequence of gene for
	.37e .38e .19e .15e .53e	5.96e-251 3.27e-192 3.27e-192 3.37e-192 9.37e-192 1.75e-192 2.19e-174 2.69e-174 2.69e-174 2.69e-174 2.69e-173 3.764e-173 3.764e-173 4.65e-159 4.31e-138 4.55e-159

## ALIGNMENTS

Qu Ma	888888888	CCCPPTTR	XXOOR KAGG	RESULT ID Q AC Q DT 0 DE E KW t
Query Match Best Local : Matches 4:	Q24441. The cytopl regulation sequesteridiseases, graft vers arthritis. See also Q Sequence	WPI; 92 P-PSDB; New pol first t treatir Example This se derivat	malaria; vir autoimmune d Homo sapiens W09207076-A. 30-APR-1992: 18-OCT-1991; 18-OCT-1990; (CHAR-) CHAR-	LT 1 Q24441; Q24441; O5-NOV- Encodes tumour i
Simil 25;	Q24441. This derivative lacks the 81 carboxyl terminal residues of the cytoplasmic domain. The derivative could be used in the regulation of TNF-alpha mediated responses by binding and sequestering human TNF-alpha e.g. in the treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis, graft versus host disease and autoimmune diseases, esp. rheumatoid arthritis.  See also Q24440-51, R24000, R24080-84, R27585, Q29236-8 Sequence 608 BP; 148 A; 159 C; 165 G; 136 T;	WPI; 92-167156/20.  WPI; 92-167156/20.  WPPSDB; R24080.  New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.  Example; Fig 7: 43pp; English.  This sequence encodes the designed TNF-alpha 55kD receptor derivative, as present in pTNFRecd. This was produced as described the designed TNF alpha 55kD receptor derivative, as present in pTNFRecd.	malaria; viral meningits; graft versus host disease; autoimmune disease; rheumatoid arthritis.  Homo sapiens.  W09207076-A.  30-APR-1992.  10-CCT-1991; G01826.  18-CCT-1991; GB-022648.  18-CCT-1990; GB-022648.  CCHAR-) CHARING CROSS SUNLEY RES CENT.  CCHAR-) CHARING CROSS SUNLEY RES CENT.	77 1 Q24441 standard; DNA; 608 BP. Q24441; 05-NOV-1992 (first entry) D5-NOV-1992 (first entry) Encodes truncated TNF-alpha 55kD receptor (197 amino acids). tumour necrosis factor alpha; extracellular binding domain; treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
7	erivative domain refalph man TWF control of the con	/20. s capabl steine-r mmune di 43pp; encodes present	meningi base; rh 1826. 3-022648 3 CROSS	1; DNA; first en ced TNF- s factor nonary d
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Score 424; DB 4; L Pred. No. 1.67e-282; 0; Mismatches 1;	the 81 orivative ed responded in 1 ifection autoimm 159 C.	le of binding human TNF alpha - comprish subdomains of TNF alpha receptor isease, septic shock, HIV etc. English. the designed TNF-alpha 55kD receptor the designed TNF-alpha 55kD receptor to pTNFRecd. This was produced as d	aft versu: id arthrii id srthrii RES CENT	kD rece extrace septic
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                                DNA encoding TNF binding protein and TNF- receptor - used in the tumour treatment and to understand mechanismsm to TNF action Disclosure; Fig 1(1-3); 51pp; German.

CD pINF-BPL5 is one of 30 positives clones in a screened cDNA library from induced TNF-induced fibrosarcoma cells. A TNF-BP had been isolated from the urine of patients with uraemia and probes/primers were constructed from the determined amino acid sequence.

To produce a vector expressing a soluble form of TNF-binding protein, this plasmid was cut with XmmI, amplified by PCR and the amplified DNA cut with BamHI and EcoRI.

CThe resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19 with BamHI and EcoRI, and the recover pTNF-BP. This was cut with BamHI and EcoRI, and the recovered fragment inserted into PAD-CMY1 (OBG283) to give the required plasmid pADTNF-BP.

See also Q06283-1 to give the required plasmid pADTNF-BP.

Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T;
   Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                       /*tag= a
/product=TNF-BP
EP-393438-A.
                                                                                                                                                                          21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT.
Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa WPI; 90-321987/43.
P-BCDB. BOTALO
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Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
pTNF-BP15; ss.
                                                                                                                                                                                                                                                                                                                       Q06282 standard;
Q06282;
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l Similarity 99.8%;
425; Conservative
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213..1325
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Pred. No. 1.67e-282;
0; Mismatches 1;
                  Length 1334;
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/product= hr:
sig_peptide
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26-MAR-1993;
30-MAR-1992;
TNF-R-linker-TNF-R-linker-IL-1R
                                                                                 WPI; 93-336592/42.
P-PSDB; R42059.
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W09319777-A.
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29-APR-1994
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30-MAR-1993; U02938.
30-MAR-1992; US-860710.
(IMMY) IMMUNEX CORP.
Smith CA;
WPT. ~~
New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Disclosure; Page 57-59; 85pp; English.

The sequences given in Q49931-32 encode human tumour necrosis fact receptor (TWF-R) and the sequences in Q49933-34 encode human interleukin-1 receptor (IL-IR). These sequences were used in the production of a fusion protein which conformed to one of the formulae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lambda-derived TNF-R cDNA.

Human; tumour necrosis factor receptor: TNF-R; interleukin-1 reception: TL-1; cachexia; cerabral mala: IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerabral mala: rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; put verses host disease; sepsis; inflammation; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATAGTGTGTCCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
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Location/Qualifiers
1..1366
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Matches 42
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/product= hu
mat_peptide
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/note= "3"
mat_peptide
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and autoimmune dysfunctions.

Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T;
                                                                                                                                                                                          024440 standard; DNA; 2062 BP. 024440; 05-NOV-1992 (first entry) 05-NOV-1992 (first entry) Encodes TNF-alpha 55kD receptor tumour necrosis factor alpha; extracellular binding domain; treatment; pulmonary diseases; septic shock; HIV infection; malaria; viral meningits; graft versus host disease;
                                                                                                                                                                                autoimmune
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The linker may com
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425; Conse
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seq:"TGG",
                                                                                                    human
                                                                                                                                                                                disease; rheumatoid arthritis
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larity 99.8%;
Conservative
                                                                                                                                Location/Qualifiers 156..1517
                                                                                 TNF-alpha
1265..1267
                                1265..1267
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Pred. No. 1.67e-282;
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               TCCTGT 770
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FI first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.

PS Claim 4: Fig 1: 43pp; English.

CC This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA control of the problem of the control of the control of the problem of the problem of the hybridising clones control of the control of the control of the human TNF-alpha clones were plaque purified and cDNA size determined by PAGE against an control of the colones were then come the coding region of the majority of the human TNF-alpha control of the coding sequenced. The coding region of the majority of the human TNF-alpha control of the coding sequenced as an ECORI fragment encoding 374 amino acids, and cloned into a mammalian cell expression vector, resulting in pringra. A derivative of the TNF-alpha receptor was produced by compinering a termination codon just prior to the transmembrane compinering a termination codon just prior to the transmembrane compinering a termination codon just prior to the transmembrane compinering at the primers Q29237, 8 generated a 300bp pringraced.

CC TNA sequencing confirmed this contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected contained contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected contained contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected contained contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected contained the designed DNA sequence. The TNF-
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Matches 42
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WPI; 92-167156/20.
P-PSDB; R244000
New polypeptide capable o
first three cysteine-rich
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W09207076-A.
30-APR-1992.
18-OCT-1991;
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/codon= Seq"
mat_peptide
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18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS SI
Brennan FM, Feldmann M,
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/codon= Seg:"GAC", aa:Asn
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                                                                  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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tide 1433..1435
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4, Gray PW, Turner MJC:
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Pred. No. 1.
0; Mismatc
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. No. 1.67e-282;
Mismatches 1;
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                              useful in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid arthritis
Disclosure; Fig 1; 25pp; English.
The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obtd. from a human placental cDNA library in lambda gtil using a probe (Q20974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is useful for treating diseases where TNF alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases, specifically rheumatoid arthritis. See also Q20974.
Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
/*tag= c
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15-JUN-1990; 013410.
15-JUN-1999; GB-013410.
(CHAR-) CHARING CROSS SUNLE.
Feldman M, Gray P, Turner M, Brennan WPI; 92-043513/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 5
Q20973 standard; DNA;
Q20973;
11-MAY-1992 (first er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumour necrosis factor alpha binding protein and polypeptide useful in treating cachexia, sepsis and auto immune diseases
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Tumour necrosis factor alpha; autoimmune
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                                                                                 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCCTCCTGCCAGGAG
                                            ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag
                                                                                                                                      AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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l Similarity 99.8%;
425; Conservative
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Pred. No. 1.67e-282;
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11-DEC-1989; US-450329.
07-FEB-1990; US-479661.
(SYNE-) SYNERGEN INC.
WPI: 91-073847/11.
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AU9058976-A.
24-JAN-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor inhibitor - for suppression of TNF-alpha and -beta, useful as therapeutic agent.

Disclosure: Fig 21: 142pp: English.

The sequence encodes the entire 30 kD TNF inhibitor. The clone from which the sequence was obtd. was isolated from a CDNA library prepd. from RNA form U937 cells treated with PNA/PNA. The whole gene can be inserted into expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and degenerative
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30kD TNF inhibitor precursor gene in lambda-gtl0-7ctnfbp.
Tumour necrosis factor; inhibitor; ss.
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Sequence 2088 1
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tcctgt
                            ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag
                                                                                                                                   CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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l similarity 99.8%;
425; Conservative
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Pred. No. 1.67e-282
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Matches 42
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31-AUG-1990; 116707.
12-SEP-1989; CH-003319.
08-MAR-1990; CH-000746.
20-APR-1990; CH-001347.
(HOFF) HOFFMANN-LA ROCH
Brockhaus M, Dembic Z, G
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/product= 55kD 1
EP-417563-A.
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See also Q10956.
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Insoluble tumour necrosis
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Encodes human 55kD TNF-binding protein.
Tumour Necrosis Factor: binding proteins; septic
autoimmune glomerulonephritis; lymphokine; cytoki
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Q10955;
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ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LambdaTNF-R2 encodes the complete human Thr and was used to construct a plasmid (pADTNF-R) expressing the product the sam pADTNF-B9 (g06282,06285.

See also Q06282-Q06285.

Sequence 2141 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/label=huTNF-R
EP-393438-A.
24-OCT-1990.
06-APR-1990; 10
21-APR-1989; DE
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Q06285;
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21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT
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90-321987/43.
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                                                                                                                                                    TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 35.3%;
l Similarity 99.8%;
425; Conservative
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Pred. No. 1.67e-282;
0; Mismatches 1;
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antagonising deleterious errors.

Disclosure; Fig 1: 40pp; English.

CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.

CC Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell type. The only region of the receptor whose structure affects the conducing agents, e.g. phorbol myristate acetate (PMA), depending on cell type. The only region of the receptor whose structure affects the conducing agents, e.g. phorbol myristate acetate (PMA), depending on cell type. The only region of the receptor whose structure affects the conducing agents. The spacer region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras between human p55 TNF-R and murine epidermal growth factor receptor (EGF-R) that are represented by R75007-11. This spacer region was subjected to deletion mutations (R75013-25) and substitutions are the subject of the spacer region, the most important residues are caption of these. The shedding of the receptor is independent of the side chain identity of these residues, with the exception of a limited conformation of the protein adversely effect the shedding process. The mutations shown in R75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNF-R creaments of these inhibitors can be seen in be used for enhancing TNF function.

Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;
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12-OCT-1993; IL-107268.

(YEDA) YEDA RES & DEV CO L

Batkin M, Brakebusch C, V

WPI; 95-194342/26.
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protease capable of cleaving soluble tumour necrosis (TNF) receptor - from cell-bound TNF- receptor, useful fantagonising deleterious effects of TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IT 9
Q90513 standard; DNA; 2175
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AU9475742-A.
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                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour necrosis factor receptor; TNF-R; human; murine; chimera;
                                                                                                                                                                                                                                  gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
agctgctccamatgccgamaggamatgggtcmggtggmgmtctcttcttgcmcmgtggmc
                                                                            tycaggyagtytyagagcygctccttcaccycttcagaaaaccacctcagacactycctc
                                                                                                                                                       aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac
                                                           TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                                                                                    AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                                                                                            GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404
                                                                                                                                                                                                                                                                                         Conservative
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2143..2149
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256..1623
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99.8%;
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Varfolomeev
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Pred. No. 1.67e-282;
0; Mismatches 1;
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                             Improved process for the selection of recombinant host cells expressing high level of a desired product - uses eukaryotic host cells contg. a DNA construct comprising a selectable gene Example 2: Page 36-42; 137pp; English.

A dicistronic vector (T15930) comprises a regulatory region derived from the cytomegalovirus immediate-early gene, a selectable dihydrofolate reductase gene positioned within an intron having a 5' wild-type ras splice donor site, a downstream sequence coding for an immunoadhesin, Ther-ig, capable of binding tumour necrosis factor, and a poly-A sequence. Transfection of CHO DHFR- cells and subsequent methotrexate amplification and growth of the cells in nutrient-rich medium gave Ther-ig in yields of 9.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T15931;
                                                                                                                                   1845
                                                                                                                                                                                                                                       1725 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 1784
                                                                                                                                                                                                                                                                                                                                                                   ug/ml (15-fold higher compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-1996.
28-JUL-1995; U09576.
05-AUG-1994; US-286740.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.

Recombinant host cell; dihydrofolate reductase; selectable marker;

DHFR; ras splice donor; dicistronic vector; gene expression;

immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
                  1965
                                                                                                                                                                                                                                                                                                                                            Sequence
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cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt
                                                           agctgctccaaatgccgaaaggaaatggggtcaggtggagatctcttcttgcacagtggac
                                                                                                                   tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc
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                                                                                                                                                                                                                      ttocagtgottcaattgcagcotctgcotcaatgggaccgtgcacctotcctgccaggag
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                                                                                                    TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                                                                                                            AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
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425; Conser
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.larity 99.8%;
Conservative
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Pred. No. 1.67e-282;
0; Mismatches 1;
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/product= pt
EP-568925-A.
                                                                                                                                                                                                                disease, septic shock, etc.

Claim 2: Figure 1: 17pp: English.

Modification of the tumour necrosis factor receptor by mutation or delation modulates signal transduction and/or cleavage effected by the receptor. This modulation of activity can also be achieved using effector proteins which interact with the TWF receptor.

Molecules which interact with the TWF receptor or the effector proteins can be used to treat or prevent diseases associated with TWF activity e.g. autoimmune disease; rheumatoid arthritis; graft rejection; graft vs. host disease or septic shock. They can also be used to treat overdoses of exogenous TWF.

Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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Q50870;
13-MAY-1994 (first entry)
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                                                                                                                                                                                                                                                                                                                                      Modulating activity of tumour necrosis factor receptor - using peptide(s), antibodies, etc. which interact with critical region freeptor or effector protein, for controlling auto-immune
                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-353057/45.
P-PSDB; R42197.
                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-1992; IL-101769
(YEDA ) YEDA RES & DEV
Brakebusch C, Wallach
                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-1993;
03-MAY-1992;
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effector pr
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                                                                                                                                                                         35.18;
Local Similarity 99.58;
les 424; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necrosis factor receptor coding sequence.
; tumour necrosis factor; receptor; disease; autoimmunity;
autoid arthritis; graft rejection; graft vs. host; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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   cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt
                     GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404
                                                                                                 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
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                                                                                                                                                                                       Score 422; DB 9; L
Pred. No. 4.91e-281;
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Q12215;
12-SEP-1991 (fir
                              /number= 4
polyA_signal
/*tag= m
EP-433900-A
26-JUN-1991
13-DEC-1990;
13-DEC-1990;
12-JUL-1990;
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/number= 2
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Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
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/note= "TBP-I
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/note= "TBP-I
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/note= "TBP-I
                                                                                                                                                                                                                                                                                                                                                /label- soluble_domain
/note- "may be 2 codons
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; IL-092697;
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A RES & DEV
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889..957
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850..858
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583..627
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256..1620
           & DEV CO LTD.
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Matches 42
   *tag= a
mat_peptide
/*tag= b
sig_peptide
/*tag= c
polyA_site
/*tag= d
mutation
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/note="c ->
mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant tumour necrosis factor binding protein I - prepd. by transfecting eukaryotic cells with vector contg. deoxyribonucleic acid encoding human type T TNF receptor or soluble domain Disclosure; Fig 1(D); 30pp; English.

The Tumour Necrosis Factor Binding Protein I is the soluble form of the Tumour Necrosis Factor Binding Protein I is the cell surface form of this receptor, corresp. to its extracellular domain. There is no characteristic poly(A) addition signal near the 3' end of the cDNA. The sequence ACTARA (tag m) may serve as an alternative to this signal, but with low efficiency. See also Q12212-15.

Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T;
                                                                                                                                                                                                                                                       Human chorionic gonadotropin beta subunit analogue Glycoprotein hormone; hCGB'; fertility; immuno-casi immuno-contragestive; vaccine; ds.
                                                                                                                                                                                                                                                                                                            Q14800 standard; DNA; 579
Q14800;
I1-FEB-1992 (first entry)
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l Similarity 99.5%;
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Pred. No. 4.91e-281;
0; Mismatches 2;
                                                                                                                                                                                                                                                                              immuno-castration;
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Matches 41
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07-MAY-1991; U03162.
08-MAY-1990; US-520703.
(UYNE-) UNIV MED NEW JERSEY.
Campbell RK, MOyle WR;
WPI: 91-353528/48.
P-PSDB; R15043.
           /*tag= a
/transl_except= /
sig_peptide
/*tag= b
                                                                                                                              IT 14
T13312; standard; cDNA; 836 BP.
T103212;
T03212;
26-APR-1996 (first entry)
26-APR-1996 (first entry)
Single chain gonadotropin analogue 1 coding sequence.
Single chain gonadotropin; human chorionic gonadotropin;
alpha; beta; subunit; analogue; glycoprotein hormone; fer
inhibit; stimulate; increase; lutropin; luteinising hormo
follicle stimulating hormone; FSH; vaccine; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New glyco-protein hormone analogues - for inducing fertility as immuno-castration agents, for suppressing reproductive system development and as immuno-contragestive vaccines.

Example 3: Fig 4a; 94pp; English.

The sequence is an analogue of hCG beta subunit cDNA contg. two silent mutations which eliminate restriction sites. It was prepd. from the plasmid pxMB-hCG-beta, a construct contg. the hCG beta subunit isolated from human placenta (Fiddes and Goodman) in plasmid pxMB, a derivative of pUC18 designed to facilitate cloning of glycoprotein hormones. The sequence was used as the starting construct for many mutants. (See R15061-R15125 and R15161-R15198). Sequence 579 BP; 128 A; 205 C; 151 G; 95 T;
                                                                                                                                                                                                                                                                                                                                                1143
                                                                                                                           Synthetic.
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/note="c
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larity 99.3%;
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33..92
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Pred. No. 3.68e-275;
0; Mismatches 3;
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hormone; fertility; hormone; LH; g

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403 1022 343 962

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Length 579;

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The thods for altering fertility in mammals, esp. humans - e.g. throughout for altering fertility by reducing the activity and/or levels of the activity and/or levels of the control of
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Matches 41
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17-FEB-1995; U02067.
18-FEB-1994; US-199382.
(SENS-) SENSI-TEST.
T03243 standa
T03243;
T03243;
08-MAY-1996
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strand also has a single-strand
its 5'-end; the sequence of the
5'-TCCGGATTAGCTTGAGATGGATCC-3'"
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                                                                                                                                                                                                                                                                                                           9999tcctgccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc
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DB; R86247.
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                                                              standard;
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                                                              CDNA; 836
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Pred. No. 1.73e-271;
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Whethods for altering fertility in mammals, esp. humans - e.g. restinuiating fertility by reducing the activity and/or levels of circulating glyco:protein hormones having lutropin activity producing the activity and/or levels of circulating glyco:protein hormones having lutropin activity producing glyco:protein hormones having lutropin activity produced in the second control of the single chain gonadotroph having a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a CG alpha-subunit at the C-terminus, joined by a linker of 1-16 amino acids. The analogue la was derived from analogue 1 by removing the two glycosylation sites from the alpha-subunit. The analogue has anti-luteinising hormone (lutropin) activity and can be used for facilitating ovulation, terminating pregnancy and reducing androgen secretion. The present sequence codes for analogue 1a.

So Sequence 836 BP; 166 A; 282 C; 222 G; 166 T;
                                                                                                                                                            Query Match
Best Local S
Matches 41
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/transl_except= |
sig_peptide
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mat_peptide
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/note- "nucleotides 93..527 encode amino ac
/note- "nucleotides 93..527 encode amino ac
1-145 of hGG beta-subunit; nucleotides
528..551 encode a (Gly-Ser)4 linker and
nucleotides 552..827 encode amino acids
1-92 of gonadotropin alpha-subunit lacking
the 91ycosylation sites at amino acid
positions 52 and 78"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain gonadotropin analogue la coding sequence. Single chain gonadotropin; hcg Single beta; subunit; analogue; glycoprotein hormone; fertil inhibit; stimulate; increase; lutropin; luteinising hormone; forlicle stimulating hormone; FSH; vaccine; contraceptive; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W0952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "wild-type Asn 52 codon has I
Gln codon to remove a glycosylation
Misc_difference 783..785
                                                                                                                                                                                                                                                                                                                                                                                                                                               Moyle WR;
WPI; 95-302553/39.
P-PSDB; R86259.
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17-FEB-1995; U02067.
18-FEB-1994; US-199382.
(SENS-) SENSI-TEST.
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31n codon to remove a glycosylation site"
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    231
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ggggtcctgccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc
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                                                                                                                                                                           Similarity
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33..92
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26
                                                                                                                                                                         34.0%;
                                                                                                                                                         Score 409; DB 17;
Pred. No. 1.73e-271;
0; Mismatches 4;
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n site"
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1143 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGACACCCCGATCCTCCCACAA 1199
agcettecaagcecateccgacteccggggcecteggacacccegatecteccecaa
1083 CCTTGACCTGTGACCCCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCC 1142
411 cccttgacctgtgatgacccccgcttccaggactcctcttcctcaaaggcccctccccc
1023 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTG
agetgtematgtgemetetgeegeegemeeneetgmetgegggggteecmaggmeeme 410
963 ATCCGGCTCCCTGGCTGCCCGCGCGCGTGAACCCCCGTGGTCTCCTACGCTGTGGCTCTC 1022
atccggctccctggctgcccgcgcggcgtgaaccccgtggtctccctacgccgtggctctc 350
903 GGGTCCTCCCGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 962

Search completed: Wed May 6 13:40:33 1998 Job time: 161 secs.

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Database: Database: emb1-est
1:em\_est1 2:em\_est2 3:em\_est3 4:em\_est4 5:em\_est5
6:em\_est6 7:em\_est8 8:em\_gss 9:em\_est13
genbank-est
10:gb\_est1 11:gb\_est2 12:gb\_est3 13:gb\_est4 14:gb\_est5
15:gb\_est6 16:gb\_est2 12:gb\_est8 18:gb\_est9 19:gb\_est10
20:gb\_est11 21:gb\_sts 22:gb\_est8 18:gb\_est12 24:gb\_est10
20:gb\_est11 21:gb\_sts 27:gb\_est16 28:gb\_est17
29:gb\_est14 26:gb\_est15 27:gb\_est16 28:gb\_est17
29:gb\_est18 30:gb\_est19 31:gb\_est20 Post-processing: Minimum Match 0% Listing first 45 summaries

Statistics: Mean 11.212; Variance 2.135; scale 5.252

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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0.00e+00							0.00e+00																							0.00e+00	•

## ALIGNMENTS

Comput	TITLE	REFERENCE AUTHORS	ORGANISM	DEFINITION ACCESSION NID KEYWORDS SOURCE	RESULT 1
Contact: Wilson RK WashU-Merck EST Project Washington University S 4444 Forest Park Parkwa	Parsons, J., Rifkin, L., Rohl Trevaskis, E., Waterston, R., Wilson, R. The WashU-Merck EST Project Unpublished (1995)	Deuterostomia; Choro Sarcopterygii; Choan Eutheria; Archonta; 1 (bases 1 to 601) Hillier, L., Clark, N Holman, M., Hultman,	polylinker hoste- polylinker hoste- Rsite2-Eco RI tw weeks post conce- oligo(dT) primer- [5'-TGTTACCAATCT [6'-TGTTACCAATCT [6'-TGTTACCAATCT [7'-TGTTACCAATCT [7'-TGTTACAATCT [7'-TGTTACAA	yw91b05.s1 Homo sapiens CHORICGONADOTROPIN BETA N32759 91153158 EST. EST. 5000-259569 prime	N32759
on RK ST Project liversity So Park Parkway	Waterston Waterston Cck EST Pro	; Chordata ; Choanata ; Choanata ; Prin : 0 601) : lark, N., Du	sst=DH10B (six bull) vector ve	ROPIN BETA	601 bp
Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. Wilson,R. The WashU-Merck EST Project Unpublished (1995)	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Ammiota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 601) 1 (bases 1 to 601) 1 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hillier, L., Clark, N., Mucaba, T., Le, M., Lepnon, G., Marra, M., Kucaba, T., Le, M., Lepnon, G., Marra, M.,	polylinker instruction vector pills (Figure 1) with a modified polylinker host-pH10B (ampicillin resistant) Rsited-Not I Rsite2-Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. Ist strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCGCGGATTTTTTTTT	yw91b05.sl Homo sapiens cDNA clone 259569 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);. N32759 91153158 EST. Clone-259569 primer-m13 -40 forward library-Soares placenta bronch clone-259569 primer-m13 -40 forward library-Soares placenta	mRNA
Louis, MO	es,M., Ta, Wohldm	thostomat.  ota; Mamm.  Hominid.  on, K., Ha.  Lennon.G	ant) Rsitt weeks and as primed as primed TTTTTTTTT ligated toned into rmacia).  a Coeloma: Coeloma:	(HUMAN);.	EST
63108	ann, P. and	a; Osteichthyes; alia; Theria; ae; Homo. wkins,M.,	polylinker instruction vector prilid (Finalmetra) while a modified polylinker host-pHIDB (ampicillin resistant) Raitel-Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCGGGATTTTTTTTTT	lar to gb:J00117	10-JAN-1996

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mRNA
BASE COUNT
ORIGIN
    REFERENCE
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                     GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGGGGGGGAGAGTGCACATTGACAGCT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGTCATCACAGGGTCAAGGG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCAGCACGCGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT
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                                                                                 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 537)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stops: 387
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                               yw69d04.sl Homo sapiens cDNA clone 257479 3' similar to CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
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WashU-Merck EST Project
WashIngton University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1810
Fax: 314 286 1810
                g1148250
EST.
                                            yw78h03.s1 Homo sapiens
CHORIOGONADOTROPIN BETA
N29730
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High quality sequence stops: 313
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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TGCACACGGGGCAGCCCTCCTTCTCCACAGCCANGGTTGGCATTGATGGGGCGGCACCGT
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
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Hillar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
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                                                                                                 GGGGGGAGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGTCATCACAGGTCAAGGG 136
                                                                                                                                          TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCCGGGAGTCGGATGGGCCTTGGAAGGCT 1143
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CHORICGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
N32604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
WashIU-Merck EST Project
WashIngton University School of Medi
WashIngton Parkway, Box 8501,
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ost
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalla;
Butheria; Archonta; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 564)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Mar
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 364 Source: IMAGE Consortium, LLNL free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
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The WashU-Merck EST Project
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
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/clone="259973"
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Pred. No. 0.00e+00;
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chosnata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 442)
Hillier_L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stops: 364
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.linl.gov) for further i
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                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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1. .442
/organism="Homo:
/clone="258663"
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                                                                                                                                       Eutheria; Archonta; Primates; Catarrhini; 1 (bases 1 to 473)
Hillier,L., Clark,N., Dubuque,T., Elliston Holman,M., Hultman,M., Kucaba,T., Le,M., L. Parsons,J., Rifkin,L., Rohlfing,T., Soares Trevaskis,E., Waterston,R., Williamson,A.,
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The WashU-Merck EST 
Unpublished (1995)
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larity 94.6%;
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Pred. No. 0.00e+00;
0; Mismatches 22
                                                                                                                                                  Le, M., Lennon, G., Marra, M., ., Soares, M., Tan, F., amson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                         Elliston, K.,
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human clone=258525 primer=ml3 -40 forward library=Soares placenta Bto9weeks 2NbHPBtc9W vector=pT7T3D (Pharmacia) with a modified polylinker host-H10B (ampicillin resistant). Rsitel-Not I Rsite2-Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer oligo(dT) pr
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
Location/Qualifiers
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Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

High quality sequence stops: 333

Source: IMAGE Consortium, LLML

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IMAGE Consortium (info@image.llnl.gov)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
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Unpublished (1995)
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Pred. No. 0.00e+00;
0; Mismatches 9;
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Le,M., Lennon,G., Marra,M.,
., Soares,M., Tan,F.,
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Best Local Similarity
Matches 407; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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      963
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                                                                                                                                                   GAGAGCCACGGCTTAGGAGACCACGGGGGTTCACGCCGCGGCGAAGCCANGGGAGCCGGA
                                                                                                                                                                                                                                                                       GTGGTCCTTGGG-CCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT
                                                        TGGACTCGAAGCGCAAATCGCGGGTAGTTGCACACCACCTGAGGCAGGGCGGCCAGACCC
                                                                                                                 GAGAGCCACAGCGTAGGAGACCACGGGGGTTCACGCCGCGGGGCAGCCA-GGGAGCCGGA
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WashIngton University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1800
Fax: 314 286 1810
TGGACTCGAAGCGCACATCGCGG-TAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stops: 400
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 566)
Hillier L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Richard, R., Rohlfing, T., Soares, M., Tan, F.,
Rohlfing, T., Soares, M., Tan, F.,
Rohlfing, T., Soares, M., Tan, F.,
Rohlfing, T., Soares, M., Tan, F.,
Rohlfing, T., Soares, M., Tan, F.,
Rohlfing, T., Soares, M., Tan, F.,
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Rohlfing, T., Soares, M., Tan, F.,
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Rohlfing, T., Soares, R., Soares, R., So
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CHORIOGONADOTROPIN BETA
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/clone="257551"
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148 c
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Pred. No. 0.00e+00;
0; Mismatches 12
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1202 TTATTGTGGAAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143
                                                                                                                                                                                                                      source
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                      TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
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                                                                   416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
14444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae: Metazoa: Eumetazoa: Bilateria; Coelomata; Deuterostomia: Chordata; Vertebrata; Gnathostomata; Ostelchthy Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 563)

Hillier,L., Clark,N., Dubuque,T., Eliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human clone=259380 primer=m13 -40 forward library=Soares 8to9weeks 2NDHP8to9W vector=p7773D (Pharmacla) with a mod polylinker host=DH10B (amplcillin resistant) Rsite1=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another weeks post conception. 1st strand cDNA was primed with a click post conception.
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                                                                                                                                                                                                                                                                                    High quality sequence stops: 335
Source: IMAGE Consortium, LLNL
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Similarity 97.0%;
416; Conservative
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                                                                                                                                                                  /organism="Homo sapiens"
/clone="259380"
<1. .>563
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                                                                                                                                                                                                                                    Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
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                                                                                                          Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os Sarcoptery911; Choanata; Tetrapoda; Amniota; Mammalla; Eutherla; Archonta; Primates; Catarrhini; Hominidae; H 1 (bases 1 to 479)
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405; Conser
                                                                                    Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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larity 97.6%;
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The WashU-Merck EST Project Unpublished (1995)
human clone=258890 primer=m13 -40 forward library=Soares placenta 8to9weeks 2NbHp8tc9W vector=pT7T3D (Pharmacla) with a modified polylinker host-DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I oligo(dT) primer
                                                                                                                                                                                                                yw84a02.s1 Homo sapiens cDNA clone 258890 3' CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMP
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
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WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
Eax: 314 286 1810
Exact School of Medicine
University School of Medicine

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llarity 95.5%;
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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WashIngton University School of Medicine
4444 Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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larity 94.1%;
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Pred. No. 0.00e+00;
0; Mismatches 21
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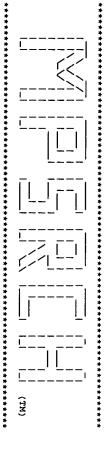
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196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGAT 254
                                                                                                                                                                                                                                                                          30.28;
Local Similarity 96.78;
les 407; Conservation
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                                      GTGGTCCTTGGGACCCCGACAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos. Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyle, T., Waterston, R. and Wilson, R. Washu, NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School
4444 Forest Park Parkway, B
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Pooled human pregnant uterus"
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Pred. No. 0.00e+
0; Mismatches
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Mismatches 8;
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 834 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 361.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos. Kucaba, T., Lacy, M., Le, N., Lennon, G., Maxra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Yootobrata: Mammalia; Eutheria; Primates; Catarrhini; Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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                                                                                                         /organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT773D-Pac
/note="Organ: mixed (see below); Vector: pT773D-Pac
/(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Ecc RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/tissue_type="Pooled human
pregnant uterus"
                                                               /db_xref="taxon:9606"
/clone="666438"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 531)
1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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l Similarity 97.2%;
375; Conservative
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EST.
                                                                                             Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                               zd66b03.sl Soares fetal heart NbHH19W Homo sapiens 3455813' similar to gb:J00117 CHORIOGONADOTROPIN B
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/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin re
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/clone="345581"
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Search completed: Wed May 6 13:37:32 1998 Job time: 1115 secs.



Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:56:17 1998; MasPar time 9.51 Seconds 482.526 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-804-166-4 (1-307) from US08804166.pep 2341 1 SRTSLLLAFGLLCLPWLQEG.....

Sequence: SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150 Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 32.496; Variance 135.826; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	ID  W33358  W33360  W33357  W33359  R24080  R70108
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 307; Conservative

Score 2341; DB 26; Pred. No. 9.21e-224; 0; Mismatches 0;

Length 307; Indels

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Gaps

0

1124 48.0 1245 13 R70106 TNF-R-P1. vivax Duffy 1124 48.0 1604 13 R70105 TNF-R-EBA 175 fusion 1118 47.8 433 R R51032 Mutant p55 tumour nec 1118 47.8 455 R R51033 Mutant p55 tumour nec 1118 47.8 455 R R51034 Mutant p55 tumour nec 1110 47.4 455 R R51034 Mutant p55 tumour nec 1110 47.4 455 R R42197 Type I TWF receptor. 1110 47.4 455 R R15174 PNG methionine substit 1021 43.6 145 R15174 PNG methionine substit 1021 43.6 145 R15174 PNG methionine substit 1021 43.6 145 R15170 PNG/PLH chimera, A5. 1020 43.6 145 R15170 PNG/PLH chimera, A3. 1020 43.6 145 R15169 PNG/PLH chimera, A3. 1020 43.6 145 R15169 PNG/PLH chimera, A3. 1020 43.6 145 R15169 PNG/PLH chimera, B3. 1021 43.6 145 R15169 PNG/PLH chimera, B3. 1022 43.6 145 R15169 PNG/PLH chimera, B3. 1023 43.6 145 R15173 PNG Mistidine substit 1024 43.6 145 R15173 PNG Mistidine substit 1025 A3.4 145 R15173 PNG Mistidine substit 1016 43.4 145 R15173 PNG Mistidine substit 1017 43.3 145 R15103 PNG PNISITIONIC gonadotroph 1018 43.3 145 R15103 PNG PNISITIONIC gonadotroph 1019 43.3 145 R15103 PNG PNISITIONIC gonadotroph 1010 43.3 145 R15103 PNG PNISITIONIC gonadotroph 1011 43.3 145 R15103 PNG PNISITIONIC gonadotroph 1012 A3.3 145 R15103 PNG PNISITIONIC gonadotroph 1013 A3.3 145 AW27682 Chorionic gonadotroph 1013 A3.3 145 AW27682 Chorionic gonadotroph
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CC A novel fusion protein comprises 2 dimer forming co-expressed amino CC acid sequences, each consisting of a homodimeric or heterodimeric CC receptor chain or ligand, with ligand-receptor binding activity, CC bound directly or via a peptide linker to a subunit of a CC the hormone's other subunits. The fusion protein, e.g. the thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit CC (hCG-beta) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone CC component, reducing the requirement for hormone itself and the CC number of injections needed.
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WPI; 97-425036/39.
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20-FEB-1996; US-011936
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Conservative
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Pred. No. 4.77e-191;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybrid dimeric protein comprising two co-expressed units - each probased on receptor or ligand and a subunit of a heterodimeric hormone, especially FSH, for inducing follicular maturation Example; Pages 32-33; 60pp; English.

Can novel fusion protein comprises 2 dimer forming co-expressed amino caid sequences, each consisting of a homodimeric or heterodimeric creceptor chain or ligand, with ligand-receptor binding activity, common comprises 2 dimer forming co-expressed amino caid sequences, each consisting of a homodimeric or heterodimer with ligand-receptor binding activity, common directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the thrombopoletin (TPO)/human chorionic gonadotrophin-alpha subunit (DG-alpha) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone component, reducing the requirement for hormone itself and the component, reducing the requirement for hormone itself and the componence 256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 16
                                                                              TBP(20-190)/hCG-alpha fusion pro
Fusion protein; thrombopoietin;
alpha subunit; hCG-alpha.
Homo sapiens.
WO9730161-Al.
21-AUG-1997.
20-FEB-1997; U02315.
20-FEB-1996; US-011936.
                                                                                                                                                                                                                 W33359 standard; Protein; W33359; 19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISTF ) ARS APPLIED RES:
Campbell RK, Chappel SC,
WPI: 97-425036/39.
N-PSDB; T94007.
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20-FEB-1997; U02315.
20-FEB-1996; US-011936.
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WO9730161-A1.
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Similarity 98.8%;
169; Conservative
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Pred. No. 1.84e-119;
                                                                                                                                                                 in; TPO;
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Whybrid dimeric protein comprising two co-expressed units - each plased on receptor or ligand and a subunit of a heterodimeric based on receptor or ligand and a subunit of a heterodimeric romance, especially FSH, for inducing follicular maturation sexample; Pages 37-38; 60pp; English.

A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric receptor binding activity, bound directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit (hGG-alpha) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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            Claim 54; Fig 2; 100pp; English.

The sequence shows a native 30 kb TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols. may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmoxinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor; ethylene glycol; pharmokinetic; adult respiratory distress syndrome; rheumatoid arthritis; septic shock; pulmonary fibrosis; spacer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            component, reducing the requirement for hormone itself and the number of injections needed.
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                                                                                                                                                                                                                                                            mediated diseases, e.g. adult respiratory distress syndrome rheumatoid arthritis, septic shock etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R27496 standard;
R27496;
                                                                                                                                                                                                                                                                                                                 New ethylene glycolated polypeptide(s) with improved pharmacokinetic properties - for treating e.g. TNF a
                                                                                                                                                                                                                                                                                                                                                          (SYND) SYNERGEN INC. Armes LG, Brewer MT, WPI; 92-348933/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-1992; U02122.
15-MAR-1991; US-669862.
17-JAN-1992; US-822296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Native 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nlfqcfnctlclngtvhlscqekqntvctchagfflrenecvscs 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120
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                                                                                                                                                                                                                                                                                                                                                                            Brewer MT, Evans RJ, Kohno T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kD TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.1%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1289; DB 26;
Pred. No. 3.29e-116;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                            Thompson RC;
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              RESULT
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Best Local Similarity
Matches 142; Conse
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 142; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Truncated TNF-alpha 55kD receptor.
tumour necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
malaria; viral meningits; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                         This sequence is a truncated TNF-alpha receptor derivative, as encoded in pTNFRecd. This was produced as described in Q24440. This was produced as described in Q24440. This derivative lacks the 81 carboxyl terminal residues of the cytoplasmic domain. The derivative could be used in the regulation of TNF-alpha mediated responses by binding and sequestering human TNF-alpha e.g. in the treatment of pulmonary diseases, septic shock, HTV infection, malaria, viral meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS SUNLEY RES CENT.
Brennan FW, Feldmann M, Gray FW, Turne
WPI; 92-167156/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
W09207076-A.
R70108 standard; Protein; 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating autoimmune disease, septic shock, HIV etc. Example; Fig 7; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q24441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                  See also Q24440-51,
Sequence 199 AA;
                                                                                                                                                                                                                                                                                                                                             graft versus host disease and autoimmune diseases, esp. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1992
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                                                           143
                                                                                      161
                                                                                                                                               101
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                                                                       kqntvctchagfflrenecvscs 183
                                                                                                                                   scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
                                                                                                                                                                                              dsvcpqgkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kqntvctchagfflrenecvscs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dsvcpqgky1hpqnns1cctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                   SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                                                                                                                                                                               DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KONTYCTCHAGFFLRENECYSCA
                                                         KONTVCTCHAGFFLRENECVSCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 AA;
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                                                                                                                                                                                                                                                     48.0%;
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99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also R27495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                R24000,
                                                                                                                                                                                                                                     Score 1124;
Pred. No. 1.
1; Mismatc
                                                                                                                                                                                                                                                                                                                R24080-84,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1124; DB 5;
Pred. No. 1.82e-99;
1; Mismatches 0
                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165
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                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                     DB 4;
L.82e-99;
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                                                                                                                                                                                                                                                                   Length 199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PT a receptor peptide.

PS Example A; Page 54-55; 93pp; English.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite

CC (Plasmodium falciparum) peptide (capable of binding to a red blood

CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples

CC of these hybrid peptides. R70108 is a fusion of tumour necrosis factor

CC receptor (in accordance with H Loetscher et al cell, vol. 61, 351-359)

CC and glycophorin binding protein (GBP) homologue (GBPH). The

CC cytokine can bind harmlessly to the RBC without deleterious effect.

CC The RBC protects the hybrid peptides from excretion from the kidney, and

CC due to steric hindrance prevents the cytokines binding to a receptor in

CC used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA

CC (pre major merozoite surface antigen) and the Duffy binding receptor

CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to

CC pref. glycophorin A, B and C, sialo glycoproteins, found on the surface

CC of RBCs. The hybrid peptides are thus used to lower the levels of free

CC cytokines in the circulation to reduce pathological damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 142; Conse
Homo sapiens.
EP-393438-A.
24-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09506737-A.
09-MAR-1995
01-SEP-1994; G01900.
03-SEP-1994; GB-018350.
23-AUG-1994; GB-017021.
(PREN/) PRENDERGAST K F.
                                                                                   Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
pTNF-BP15; infectious disease; parasitic disease; cachexia;
autoimmune disease; shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1995 (first entry)
10-NOV-1995 (first entry)
TNF-R-GBPH fusion protein.
Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cytokine receptor; glycophorin binding peptide 130; GBPH 130; GBPH; glycophorin binding peptide homologue; glycophorin A; tumour necrosis factor receptor; TNF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prendergast KF;
WPI; 95-115452/15.
New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell
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Chimeric Plasmodium falciparum
                                                                                                                                                                                                        R07449;
29-JAN-1991 (first
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10-NOV-1995
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                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.0%;
llarity 99.3%;
Conservative
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/note= "can be repeated n
number"
                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                    371
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Pred. No. 1.82e-99;
1; Mismatches 0;
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TRESULT OF CHRISH SEED OF SECOND SEED OF SEED 
PT a receptor peptide.

PS Example A; Page 53-54; 93pp; English.

CC (Pibrid peptides for binding cytokines, comprising a malaria parasite CC (Pibrid peptides for binding cytokines, comprising a malaria parasite CC (Plasmodium falciparum) peptide (capable of binding to a red blood CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples CC of these hybrid peptides. R70107 is a fusion of tumour necrosis factor CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) CC and glycophorin binding protein (GBP) 130. The use of cytokine can bind CC receptors not normally found on RBCs means that the cytokine can bind CC harmlessly to the RBC without deleterious effect. The RBC protects the CC hybrid peptides from excretion from the kidney, and due to steric CC hindrance prevents the cytokines binding to a receptor in another cell. CC GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides cc used, others include EBA 175 (175 kDa erythrocyte binding antigen), common control of the complex control of the control o
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                red blood cell; cytokine rec
GBP 130; GBPH; glycophorin b:
Chimeric Homo sapiens.
Chimeric Plasmodium falciparu
WO9506737-A.
09-MAR-1995.
01-SEP-1994; G01900.
03-SEP-1994; GB-018350.
23-AUG-1994; GB-017021.
(PRENY) PRENDERGAST K F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanismsm to TNF action bisclosure; Fig 1(1-3); Slpp; German.

Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of e.g. CO57 cells. The expressed proteins are useful prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock, cachexia, autoLumune diseases, adult respiratory distress syndrome etc., or side effects of treatment with TNG-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 95-115452/15.

New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cytokine receptor; glycophorin binding peptide 130; caphorin binding peptide homologue; glycophorin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R70107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1995 (first entry)
TNF-R-GBP 130 fusion prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q06282.
DNA encoding TNF binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hauptmann R, Himmler WPI; 90-321987/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prendergast KF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See ālso Q06282-Q06285.
Sequence 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
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Pred. No. 1.82e-99
1; Mismatches (
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RESULT PRODUCT NAME OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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Best Local S
Matches 14
                                                                         The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion prottien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosts and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, Theumatoid arthitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Disclosure; Page 57-59; 85pp; English.

The sequences given in R42058-59 repressent human tumour necrosis factor receptor (TNF-R) and the sequences in R42060-61 represent human interleukin-1 receptor (IL-IR). These sequences were used in the production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft verses host disease; sepsis; inflammation; allergy; graft.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R42059 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor molecule (eg. exhibited by Plasmodium vivax). These peptides bind to pref. glycophorin A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid peptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                            diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses
                                                                                                                                                                                                                                                                                                                                       TNF-R-linker-TNF-R
                                                                                                                                                                                                                                                                                                                                                                 TNF-R-linker-TNF-R-linker-TL-1R
IL-1R-linker-TNF-R-linker-TNF-R or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-1993; U02938.
30-MAR-1992; US-860710.
(IMMV) IMMUNEX CORP.
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41..455
/note= "Mature hmwn.~"
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Pred. No. 1.82e-99;
1; Mismatches 0
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RESULT 12
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DE TNF-alpha bin
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Matches 14
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Best Local S
Matches 14
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Disclosure; Fig 21; 142pp; English.

The sequence comprises the entire 30 kD TNF inhibitor. The cloffrom which the sequence was deduced was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA. The whole gene can be inserted into expression vectors for proof TNF inhibitor for use in the treatment of inflammatory and degenerative diseases. The active protein is claimed (Claim Control of TNF inhibitor for use in the treatment of inflammatory and degenerative diseases. The active protein is claimed (Claim Control of TNF inhibitor for use in the treatment of inflammatory and degenerative diseases. The active protein is claimed (Claim Control of TNF inhibitor for use in the treatment of inflammatory and degenerative diseases. The active protein is claimed (Claim Control of TNF inhibitor for use in the treatment of inflammatory and degenerative diseases.
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R10986
R10986;
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18-JUL-1989; US-381080.
11-DEC-1989; US-450329.
07-FEB-1990; US-479661.
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larity 99.3%;
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Pred. No. 1.82e-99;
1; Mismatches 0
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Pred. No. 1.82e-99;
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Disclosure; Fig 1; 25pp; English.
The amino acid sequence is that of tumour necrosis factor alpha binding protein which contains the extracellular domain of human TNF alpha receptor. It is soluble and can be used in the regulation of TNF-mediated responses by binding and sequestering the cytokine. It can therefore be used therapeutically to treat disorders such as
                                                                                                                                                                                                                                                                                 R75084 standard;
R75084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHAR-) CHARING CROSS SUNLE. Feldman M, Gray P, Turner M, WPI; 92-043613/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                            epidermal growth factor
                                                                                                                                                                                                                                                p55 TNF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New tumour necrosis factor alpha binding protein and polypeptide useful in treating cachexia, sepsis and auto immune diseases
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                                       modified_site
                                                                      modified_site
                                                                                                          modified_site
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                            phorbol myristate acetate;
                                                                                                                                                                                                                                                                19-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therefore be used
hexia, sepsis and
                                                                                                                                                                                                            tumour necrosis factor receptor; TNF-R; human;
ermal growth factor receptor; EGF-R; protease; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCSKCTKEM9qve1ssctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
                                                                                                                                                                                                                                                                                                                                                                                         kqntvctchagfflrenecvscs 183
                                                                                                                                                                                                                                                                                                                                                                                                                                      SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
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larity 99.3%;
Conservative
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                                     /note=
                                                                                                      /note= "N terminus of 54..56
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                                                                       145..147
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                                                                                    /note= "glycosylation
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                                                                                                                                                                                                                                                                                                   Protein;
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                                   e= "glycosylation site".163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "transmembrane domain'
                   "glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential N-glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1124;
Pred. No. 1.
1; Mismatc
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CC Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different inducing agents, e.g. phorbol myristate accetate (PMA), depending on cell type. The only region of the receptor whose structure affects the shedding response is the spacer region (see R75012) in the extracellular combination of the spacer region (see R75012) in the extracellular domain. This region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras between human p55 TNF-R and murine epidermal growth factor receptor (RSF-R) that are represented by R75017-11. This spacer region was subjected to deletion mutations (R75013-25) and substitutions (R75016-47). Of the spacer region, the most important residues are (R75026-47). Of the spacer region, the most important residues are comportant of these. The shedding of the receptor is independent of the side chain identity of these residues, with the shedding the most conformation of the protein adversely effect the shedding process. The mutations shown in R75013-47 were introduced in order to create an conformation of a protease that is capable of cleaving the soluble TNF-R from the cell bound TNF-R. Fragments of these inhibitors can be seen in CC concerns a fragments of these inhibitors can be seen in CC concerns and a region of the second of rephancing TNF function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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12-OCT-1993; IL-107
(YEDA ) YEDA RES 6
Batkin M, Brakebus
WPI; 95-194342/26.
                                                                                                                                R07451;
Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert. Tumour necrosis factor binding protein; TNF-BP; TNF-receptor; infectious disease; parasitic disease; cachexis; autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New protease capable of cleaving soluble tumour necrosis (TNF) receptor - from cell-bound TNF- receptor, useful fantagonising deleterious effects of TNF.
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                                                                                                                                                                                                                                                                                                                    161 kqntvctchagfflrenecvscs
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                                                                                                                                                                                                                                                                                                                                                                                                      scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe
                                                                                                                                                                                                                                                                   KONTVCTCHAGFFLRENECVSCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                           SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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                                                                                                                                                           standard;
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203
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201
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202
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198..210
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Varfolomeev
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Pred. No. 1.82e-99;
1; Mismatches 0
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C raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.

LiambdaTNF-R2 encodes the complete human TNF-R2 and was used to construct a plasmid (pADTNF-R) expressing the product the same way as pADTNF-BP (see Q06282). The expressed proteins are useful prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock, cachexia, autoimmune diseases, adult respiratory distress syndrome etc., or side effects of treatment with TNG-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions.
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Best Local Similarity 99.3%;
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                                                                                              EP-417563-A.
20-MAR-1991.
31-AUG-1990;
12-SEP-1989;
08-MAR-1990;
20-APR-1990;
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06-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT.
                     (HOFF ) HOFFMANN-LA ROCHE AG.
Brockhaus M, Dembic Z, Gentz
Schlaeger EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1991 (first entry)
Human 55kD TNF-binding protein.
Tumour Necrosis Factor; binding proteins; septic shock;
autoimmune glomerulonephritis; lymphokine; cytokine.
                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                   region
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WPI; 90-321987/43.
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; CH-003319.
; CH-000746.
; CH-001347.
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151
                                                                                                                                                                                                                                                             'label-
                                                                                                                                                                                                                                                                                                           'label- transmembrane region
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Matches 14
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Claim 1; Fig 1; 26pp; German.

Partial amino acid sequences were determined for the 55 and 75kD

TNF-BPs (see R11072-R11081) and oligonucleotide primers were
synthesised based on these partial sequences. The primers were used
to produce a cDNA fragment for use as aprobe to screen a human
placental cDNA bank constructed in lambda gt11. Positive clones were

NNA constructs comprising the TNF-BP coding
                                                                                                                                                                                                                                                                                                                            sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer improved INF-binding properties.
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Claim 1; Fig 1; 26pp;
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Insoluble tumou
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                                                                                                                                                                                                                                    Local Similarity 99.3%;
nes 142; Conservative
                                                                                                                                                                      dsvcpqgkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
                                                             kqntvctchagfflrenecvscs
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                                             KONTVCTCHAGFFLRENECVSCA
                                                                                                         SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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Мау
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08:57:56 1998
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Pred. No. 1.82e-99;
1; Mismatches 0;
                                               165
                                                                          183
                                                                                                                                                                                                                                                               Length 455;
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed May 6 08:55:24 1998; MasPar time 13.64 Seconds 821.959 Million cell updates/sec

Title: >US-08-804-166-4 (1-307) from US08804166.pep 2341

Description: Perfect Score: Sequence: 1 SRTSLLLAFGLLCLPWLQEG......PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150 Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 \ 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 42.076; Variance 82.446; scale 0.510

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

22 23 23	115 115 116 118	11111 0887654 11110	Result No.
614 613 596	740 709	1124 1124 1118 11114 11105 1098 1098 1030 1030 1030 1034 955 841	Score
	33333333333333333333333333333333333333	8877774444460000000000000000000000000000	Query Match 1
141 141 169 119	461 110 110 110 121	0.000000000000000000000000000000000000	Length [
2121		- 2 - 2 2 2 2 2 2 2 2 2 2 2 2 2	BB
UTBOB 146949 KTHOB A61465	GQETT1 1XULB 1HCNB 1HCNB 1HRPB 137994 UTHUB	1EXTB GQHUT1 1EXTA 1NCFB 1INRR 11VRR 137412 KIHUB 137231 KIHUB 137231 JC4302 KIBAB 157826 GDMST1	ID
beta ing h nadoti beta	ინდიდ	tumor necrosis factor beta gonadotropin be beta gonadotropin be beta gonadotropin be beta gonadotropin be choriogonadotropin be tumor necrosis factor tumor necrosis factor	Description
1 1 1 1	2.19e-14/ 2.19e-139 4.02e-139 4.02e-139 4.02e-139 6.96e-126 2.16e-119	2.76e-207 2.76e-207 2.76e-207 3.78e-206 3.78e-203 9.0e-202 3.16e-187 3.16e-187 3.16e-186 2.83e-150 2.83e-150 3.90e-147	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
350	357	361	366	388	398	403	405	407	411	416	420	426	427	430	582	585	587	594	595	597	598
15.0	15.2	15.4	15.6	16.6	17.0	17.2	17.3	17.4	17.6	17.8	17.9			18.4						25.5	
159	166	147	158	142	142	140	112	113	142	142	119	146	141	144	141	118	138	141	118	141	141
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151373	I51242	I50994	A61091	I50143	A25800	A48166	S21196	S07092	I51232	C36179	S09344	S16763	B60626	UTCAB	JC4527	PN0141	S00512	UTSHB	PN0139	UTRTB	UTPGB
luteinizing hormone b	luteinizing hormone b	gonadotropin II beta	lutropin beta chain p	gonadotropin II beta	gonadotropin beta cha	gonadotropin II beta	lutropin beta chain -	gonadotropin beta cha	gonadotropin II beta	gonadotropin II beta		gonadotropin beta cha	beta	gonadotropin beta cha	luteinizing hormone b	lutropin beta chain -	lutropin beta chain p	lutropin beta chain p	beta	lutropin beta chain p	lutropin beta chain p
4.51e-46	1.89e-47	3.09e-48	3.18e-49	1.39e-53	1.42e-55	1.42e-56	5.68e-57	2.26e-57	3.58e-58	3.57e-59	5.64e-60	3.52e-61	2.22e-61	5.53e-62	5.41e-93	1.30e-93	5.02e-94	1.80e-95	1.12e-95	4.31e-96	2.67e-96

## ALIGNMENTS

RESULT

68-70 143-145 9-11, 19-21 133-136, 139-142 133-131, 139-142 27-31, 41-44 73-76, 85-87 92-98, 101-106 113-117, 126-129 5-19	Resolu Determ R-valu	REFERENCE #authors #journal #title	rs al	PUB_ITILE EXTRACELLULA  receptor.  ORGANISM #formal_name #note residues 1  receptor.  receptor.  receptor.  receptor.  receptor.  expression  **Expression  **authors Naismith, J.  **submission submitted to  **cross-references PDB:IEXT  REFERENCE TN026251	
<pre>#region helix (right hand 3-10)\ #region helix (right hand 3-10)\ #region beta sheet\ 2 #region beta sheet\ /pre>	complex: implication on e; signalling prot	or. ; Janes, W.; Gentz, R.; Sc. scher, H.; Lesslauer, W. soluble human 55 kd TNF	Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R. J. Biol. Chem. (1995) 270:13303 Crystallographic evidence for dimerization of unliganded tumor necrosis factor receptor.  TNO26252 TNO26252 Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale, K.; Naismith, J.H.; Sprang, S.R. J. Mol. Biol. (1994) 239:332 Two crystal forms of the extracellular domain of type i tumor	receptor crystallized at ph3.7 in p 21 21 21 and receptor crystallized at ph3.7 in p 21 21 21 and #formal_name Homo sapiens #common_name man expressed in Escherichia coll, the construct contains residues 12 to 17.2 of the mature sequence of the entire receptor residue 11 is mutated to met as a result of the expression system A65560 Naismith, J.H.; Sprang, S.R. submitted to the Brookhaven Protein Data Bank, July 1996 ces pdB:IEXT TNO26251	1EXTB #type complete tumor necrosis factor receptor extracellular domain, chain B

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##molecule_type DNA
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143-156
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##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;
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Similarity 99.3%;
                                                                                                                                                                                                                         M.; Tabuchi, H.; Lesslauer, W. Cell (1990) 61:351-359
Molecular cloning and expression necrosis factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                 Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F. Genomics (1992) 13:219-224
Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to chromosome 12p13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding protein 1 (TNF blocking factor)
#formal_name Homo sapiens #common_name man
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor necrosis factor receptor type 1 precursor - humanAlTERNATE_NAMES tumor necrosis factor alpha inhibitor; tumor necrosis factor
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Pred. No. 2.76e-207;
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                           receptor for human
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#title Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.
#cross-references MUID:90292116
#accession A60231
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##molecule_type mRNA
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Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
Stratowa, C.; Adolf, G.R.

#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor
necrosis factor receptor chain (p60) and its soluble
derivative, tumor necrosis factor-binding protein.
#cross-references MID:91090841
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##molecule_type mRNA
##residues 1-455 ##label GRA
##cross-references GB:M37764
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*accession S12057
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#title Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protein.
#cross-references_MUID:91017509
                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues 1-13 ##label KEM
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**cross-references GB:M63121; NID:g339755; PID:g339756

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#residues 1-455 ##label SCH
##cross-references GB:M33294; NID:g339744; PID:g339745
                 ##molecule_type
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30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
##residues 107-128;162-167,'X',169-201 ##label HI2
the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the receptor
                                                                                                                                                                                                                                                                                                                                                                             Kemper, O.; Wallach, D.
Gene (1993) 134:209-216
Cloning and partial characterization of
human p55 tumor necrosis factor (TNF)
JT0758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nophar, V.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwan Rophar, V.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwan R.; Aderka, D.; Holtmann, H.; Wallach, D. EMBO J. (1990) 9:3269-3278
Soluble forms of tumor necrosis factor receptors (TNF-Rs). Soluble forms for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.
                                                                                                                                                                                                          Eur. J. Immunol. (1990) 20:1167-1174
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protein
41-43,'X',45-53,'X',55-57 ##label
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m Thr}, AAG for residue 372 as Leu, and GAC for residue
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KEYWORDS
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                                              SUMMARY
    Query Match
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84-126
127-167
168-196
212-234
235-455
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#map_position 12p13.2-12p13
#introns 13/3: 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
#SUPERFAMILY tumor necrosts factor receptor type 1; NGF
receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #accession JC2404
##molecule_type protein
##residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession A35010
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J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
R.S.; Granger, G.A.

#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784

Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.

#cross-references MUID:91062364
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This protein is one of two known receptors for
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41.43,'X',45-53,'V',55-57,'XK',60
##residues
##experimental_source renal failure patient urine
NCE A35010
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##residues 41-60 ##label GAT
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##experimental_source normal urine
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Eur. J. Haematol. (1989) 42:270-275
Isolation and characterization of a tumor necrosis factor binding protein from urine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K. Biosci. Biotechnol. Biochem. (1994) 58:2266-2268 Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.
                                                                                                                                                                                                                                                                                                                                                                                   duplication; glycoprotein; receptor; transmembrane protein
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                                                                                                 #domain extracellular #status predicted #label EXT\
#product TNF binding protein 1 (tumor necrosis factor
alpha inhibitor) #status experimental #label TBP1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain transmembrane #status predicted #label NEM\
#domain intracellular #status predicted #label NEM\
#domain intracellular #status predicted #label NEM\
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                                                                                    #binding_site carbohydrate (Asn)
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    .08;
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    Score 1124;
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Length 455;
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Best Local Similarity 99.3%; Matches 142; Conservative
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71-74,83-85
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Crystal structure of the soluble human 55 kd TNF
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#formal_name Homo sapiens #common_name man expressed in Escherichia coli, the construct contains expressed in Escherichia coli, the construct contains expressed in Escherichia coli, the construct contains residues 12 to 172 of the mature sequence of the entire receptor, residue 11 is mutated to met as a result of the
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J. Mol. Biol. (1994) 239:332
Two crystal forms of the extracellular domain of type i tumor
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J. Biol. Chem. (1995) 270:1330
Crystallographic evidence for
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Local Similarity 99.3%;
nes 140; Conservative
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VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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                                                                                                                                                                                                                                                                                                                                            receptor activation.
Resolution: 2.25 angstroms
Determination: X-ray diffraction
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Similarity 99.3%;
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Cell (1993) 73:431-445
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K.; Naismith, J.H.; Sprang, S.R.
J. Mol. Biol. (1994) 239:332
Two crystal forms of the extracellular domain
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to the Brookhaven Protein Data
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Pred. No. 3.78e-205;
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                                                                                                                                                                                                                                                         86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crystallization and preliminary analysis thisbeta-55 kd this receptor complex. Resolution: 2.85 angstroms
Determination: X-ray diffraction
                                                                                                                                                                                                                                                                                                                     h 47.2%;
Similarity 100.0%;
139; Conservative
tumor necrosis factor receptor 55 kd extracellular domain contains residues 12 172 of the mature receptor sequence, chain A - hu stnfr1; type i receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for receptor activation.
                                                                             1NCFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.; Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gent Lesslauer, W.
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Cell (1993) 73:431-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complex(lymphokineRECEPTOR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the Brookhaven Protein Data Bank, May ces PDB:1TNR
                                                                                                                                                                                                                                                                                                                                                                                  #length 139
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#formal_name Homo sapiens #common_name man
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th 139 #molecular-weight 15746 #checksum
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Pred. No. 3.17e-203;
0; Mismatches 0;
                                                                          complete
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23-42
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129-140
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#submission
                                                                                          #authors Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
#journal Nature (1984) 307:37-40
#title Evolution of the genes for the beta subunits of human
chorionic gonadotropin and luteinizing hormone.
#cross-references MUID:84093590
#accession 137412
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                                  ##molecule_type DNA #residues 1-145 #-
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                           ##cross-references EMBL:X00265; NID:g31719
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                                                                                                                                                                                                                                                                                                                                                                    KONTVCTCHAGFFLRENEC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor activation.

Resolution: 2.25 angstroms

Determination: X-ray diffraction

R-value: no refinement

binding protein; cytokine; signalling
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Similarity 100.0%;
139; Conservative
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137231
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H.J.; Broger, C.; Loetscher, H.; Lesslauer, W
Cell (1993) 73:431-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; E
K.; Naismith, J.H.; Sprang, S.R.
J. Mol. Biol. (1994) 239:332
Two crystal forms of the extracellular domain
                                                                                                                                                                                                                            beta-gonadotropin - human (fragment)ORGANISM 21-Feb-1997 #sequence_revision 21-Feb-1997 #1 09-May-1997
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expressed in Escherichia coli, residue 11 is
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Pred. No. 9.90e-202;
0; Mismatches 0;
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##residues 1-23,'M',25-136,'A',138-165 ##label_PO2
##cross-references_GB:K03183; NID:g180442; PID:g180444
##note clone_CG-beta-a
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                                      ##molecule_type DNA
##residues 1-5 ##label PO3
###cross-references GB:M13504; N
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                                                                                                                                                                                                                                                                                                                                                                                  ##status
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                           ##note
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1-165 ##label POL
##cross-references GB:KO3189; NID:g180450; PID:g180453
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Similarity 100.0%;
139; Conservative
                                                                                                                                        Policastro, P.F.; Daniels-McQueen, S.; Carle, J. Biol. Chem. (1986) 261:5907-5916
A map of the hCG beta-LH beta gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Policastro, P.; Ovitt, C.E.; Hoshina, M.; Fukuoka, Boothby, M.R.; Boime, I.
Boothby, M.R.; Boime, I.
J. Biol. Chem. (1983) 258:11492-11499
The beta subunit of human chorionic gonadotropin 1
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Nature (1980) 286:684-687
The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution of a gene by readthrough into the 3'-untranslated region.
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##molecule_type protein
21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP'
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#journal J. Biol. Chem. (1975) 250:5247-5258
#title The amino acid sequence of human chorionic
#cross-references MUID:75211304
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**Fauthors Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.

**Journal J. Biol. Chem. (1981) 256:1816-1823

**Title The amino acid sequences of the prepeptides contained in alpha and beta subunits of human choriogonadotropin.

**Cross-references MUID:81117268
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#accession B56873
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#journal J. Biol. Chem. (1973) 248:6810-6827
#cross-references MUID:74011267
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##residues 26-32,'X',34-49,'X',51-60;75-112 ##label BI2
##mote this material from pregancy urine lacks stalic acid in
##mote the mature form into two chains linked by disulfide
##molecule_type protein
##residues 26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X'
##residues 78-91,'G',93-102 ##label KAR
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##residues 21-165 ##label MOR
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##residues 1-20 ##label BIR
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##residues 21-165 ##label SHI
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##cross-references GB:M13503; N
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**cross-references GB:M13505; NID:g180429; PID:g463089

**note CG-beta-6 gene
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Structure of the human chorionic gonadotropin beta-subunit fragment from pregnancy urine.
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Chinese Biochem. J. (1990) 6:558-562

The immunological characteristics of the enzymatic of human chorionic gonadotropin beta-subunit.
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29-77,43-92,46-130,
54-108,58-110,
113-120 #
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                                                                                                                                 #authors Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
#journal Nature (1984) 307:37-40
#title Evolution of the genes for the beta subunits of human chorionic gonadotropin and luteinizing hormone.
#cross-references MUID:84093590
#accession 137231
#introns
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p_position 19q13.3-19q13.3
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Local Similarity 100.0%;
hes 139; Conservative
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21-Feb-1997 #sequence_revision 21-Feb-1997 #1
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Crystal structure of human chorionic gonadotropin.
annotation; X-ray crystallography, 3.0 angstroms;
of disulfide bonds
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J.W.; Canfield, R.E.; Machin, K.J.; Morgan,
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#binding_site_carbohydrate (Asn) (cova
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211-231
361-447
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#title
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cession PC4093

##molecule_type protein

1-7 ##label SU2

---- kidney cell line
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##cross-references GB:U19994; NID:g1141752; PID:g1141753
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                    161 KQDTICNCHSGFFLRDKECVSC 182
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                                                      83
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                                                                                                                                                                                                              Match 40.8%;
Local Similarity 80.3%;
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Local Similarity 99.3%;
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                                                                                                                                        ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
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                                                                                                                        DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLPSPSRLPGPSDTPILPQ 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTIDCGGPKDHPLICDDDRFQASSSSKAPPP 126
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                                                                                       SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
                                                    138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suter, B.; Pauli, U.
Gene (1995) 163:263-266
Cloning of the cDNA encoding the
factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily pituitary glycoprotein hormone beta chain
#length 145 #checksum 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein; kidney; receptor; transmembrane protein; tumor
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   receptor repeat homology
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29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
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#domain transmembrane #status predicted #label TI
#domain signal transduction #status predicted #i
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#product tumor necrosis factor receptor p55 #status
predicted #label MAT\
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1 461 #molecular-weight 50696 #checksum
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                                                                                                                                                                                          Score 955; DB 2; Length 461;
Pred. No. 2.83e-171;
16; Mismatches 12; Indels
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Best Local
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33,50
                                                               #journal Mol. Immunol. (1993) 30:165-176
#title Genomic organization and promoter func
tumor necrosis factor receptor beta
#cross-references MUID:93156721
#accession 157826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors Crawford, R.J.; Tregear, G.W.; Nial Fjournal Gene (1986) 46:161-169
#title The nucleotide sequences of baboon beta-subunit genes have diverged #cross-references MUID:87106851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-77,43-92,46-130,
54-108,58-110,
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##residues 1-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
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                                                                                                                                                                                                                                                                                                                                                                                                                                          229
##residues 1-454 ##label RES#ross-references GB:M76656; NID:g202100; PID:g202102
                                ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                     289 SLPSPSRLPGPSDTPILPQ 307
                                                      ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
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Local Similarity 81.3%;
Les 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are at least five copies of CG-related genes and at least of these are expressed in the baboon placenta.

TION #superfamily pituitary glycoprotein hormone beta chain glycoprotein; hormone; placenta; pregnancy maintenance
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#common_name olive baboon
31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
                                                                                                                                                                                                                                             tumor necrosis factor receptor - mouseORGANISM
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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                                                                                                                                                                       Rothe, J.G.;
                                                                                                                                                       Steinmetz, M.
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#binding_site carbohydrate (Asn) (covalent) #status
predicted\
#binding_site carbohydrate (Ser) (covalent) #status
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th 165 #molecular-weight 17592 #checksum 4960
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#product choriogonadotropin beta chain #status predicted
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                                                                                                                                                                         Bluethmann,
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Pred. No. 1.63e-150
14; Mismatches 1;
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                                                                                                                                                                         Gentz,
                                                   from
                                                   GB/EMBL/DDBJ
                                                                                                                      function of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 165;
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                                                                                                                                                                         R.; Lesslauer,
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is specifes specific.
#cross-references_MUID:91187885
 *cross-references
                                                                                                                                                               #accession
                                                                                                                                                                               *cross-references MUID: 91285014
                                                                                                                                                                                                                                      #journal
                                                                                                                                                                                                                                                                          *authors
                                                                                                                                                                                                                                                                                                                                                                 #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannar C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
#journal Mol. Cell. Biol. (1991) 11:3020-3026
#title Molecular cloning and expression of the type 1 and type 2
#cross-references MUID:91246168
#accession B40254
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#*residues 1-454 ##label GO2
##cross-references GB:M60468; NID:g199825; PID:g199826
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##cross-references EMBL:X59238; NID:g53578; PID:g53579
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Similarity 70.6%;
101; Conservative
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Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; K. A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J. Eur. J. Immunol. (1991) 21:1649-1656

Cloning, expression and cross-linking analysis of p55 tumor necrosis factor receptor.
                          Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics (1991) 34:338-340
Molecular cloning and expression of the mouse Inf receptor
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13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; #superfamily tumor necrosis factor receptor type 1; Kreceptor repeat homology
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MUID: 92039815
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##Cross-referencesEMBL:X57796; NID:g54848; PID:g54849
REFERENCE 154532
                                                                                                                     #authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.
Pfizenmaler, K.; Lantz, M.; Olsson, I.; Hauptmann, R.
Stratowa, C.; Adolf, G.R.
#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
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#title Nucleotide sequence of the TNF type
endothelioma cell line.
#cross-references MUID:94245292
#accession I54532
            ##residues 1-461 ##label
##cross-references GB:M63122;
                                                                 ##molecule_type mRNA
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##cross-references GB:L26349; NID:g430732; PID:g430733
This protein is one of two distantly related receptors for
TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
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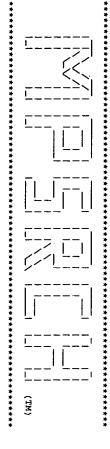
TION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                             Structure (London) (1994) 2:545
Structure of human chorionic gonadotropin at 2.6 a resolution from mad analysis of the selenomethionyl protein.

Resolution: not applicable Determination: theoretical model compelex; 91/coprotein hormone receptor glycoprotein; hormone; phosphorylation; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N. submitted to the Brookhaven Protein Data Bank, December 1996
                                                                                                                                                                                                                                                                                                                                           Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, Wu, H.; Hendrickson, W.A.; El Tayar, N.
Structure (London) (1996) 3:1341
Structural predictions for the ligand-binding region of glycoprotein hormone receptors and the nature of hormone-receptor interactions structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chorionic gonadotropin, chain B - humanPDB_TITLE receptor complexed with human chorionic gonadotropin #formal_name Homo sapiens #common_name man A66957
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predicted #label MAT\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #type complete
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Pred. No. 2.19e-140;
21; Mismatches 24; Indels
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y Match 34.3%;
Local Similarity 100.0%;
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Pred. No. 4.02e-139;
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Search completed: Wed May 6 08:55:58 1998 Job time : 34 secs.

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Run on: MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Wed May 6 08:53:11 1998; MasPar time 9.09 Seconds 846.789 Million cell updates/sec

Title: >US-08-804-166-4 (1-307) from US08804166.pep 2341

Description:
Perfect Score:
Sequence: SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150 Gap 11

Searched: 69112 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 43.895; Variance 73.304; scale 0.599

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

222221187 2322221187 23222221187	Result
11124 1035 955 857 887 740 614 613 6614 614 614 614 614 614 614 614 614 61	Score
11111222555555555555555555555555555555	Query Match Length
1455 4655 4655 1656 1654 1654 1654 1654	
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TUR1_HUMAN CGHB_PAPAN TUR1_PIG GGHB_PAPAN TUR1_MOUSE TUR1_MOUSE TUR1_MOUSE TUR1_MOUSE TUR1_RAT LSHB_HUMAN LSHB_BOVIN LSHB_BOVIN LSHB_BOVIN LSHB_BALAC LSHB_BALAC LSHB_BALAC LSHB_BALAC LSHB_BALAC LSHB_CANFA LSHB_BALAC LSHB_CANFA LSHB_CYPCA GTHB_CYPCA GTHB_CYPCA GTHB_CYPCA GTHB_CTFID GTH2_CUAGA	ID
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## ALIGNMENTS

RA RA	R R R R R	RA RA	RA RA	R R A R R R	2	88888	2 2 2 2 2 A	RESULT ID T
GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.; PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).  [6] SEQUENCE FROM N.A. MEDLINE; 92250049. FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;	·	3269-3278 ROM N.A. 1090841. MAURER-I DLSSON I.	[3] SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201. MEDLINE; 91006021. NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R., ADERKA D., HOLTMANN H:, WALLACH D.;	[2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 90235284. LOETSCHER H., PAN YC.E., LAHM HW., GENTZ R., BROCKHAUS M., TABUCHI H., LESTADUER W.; CELL 61:351-359(1990).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUB-PLACENTA;  MEDIINE; 90:35285.  MEDIINE; 90:35285.  SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,  GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;  CELL 61:361-370(1990).	RI OR THEAR.  O SAPIENS (HUMAN).  ARYOTA; METAZOA; CHORDATA; VEHERIA; PRIMATES.		TIRT 1 TIRTL_HUMAN STANDARD; PRT; 455 AA.

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DOMAIN
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                         RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR MOLECULE FADD AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTECKES) MEDIATING APOPTOSIS.

1- SUBURIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF TWENL LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERFACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. INTERFACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO THER COMPLEX BY THEIR ASSOCIATION WITH TRADD, THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KARPA B SIGNALING.

1- SUBSCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1- SIMILARITY: CONTAINS A LA-NGER/TWER-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                               EMBL;
PIR; P
PIR; S
PIR; S
PDB; 1
PDB; 1
PDB; 1
PDB; 1
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EMBL;
EMBL;
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EMBL;
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BANNER D.W., D'ARCY A., JANES W., GENTZ R.,

BROGER C., LOETSCHER H., LESSLAUER W.;

CELL 73:431-445(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENOMICS
[7]
                                                                                                                                                                                                             PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; PROSITE; PS50017; DEATH_DOMAIN;
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MEDLINE; 90110215
ENGELMANN H., NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAISHINE; 97094982.
NAISHIH J.H., DEVINE T.Q.,
STRUCTURE 4.1251-1262(1996).
-I- FUNCTION: RECEPTOR FOR 1
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                                                                                                                                                                                           3D-STRUCTURE.
                                                                                                                                                                                                      RECEPTOR; TRANSMEMBRANE;
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                                                                                                                                                                                                                                                                                           1. X55313; G37224; -...
2. X55313; G339745; -...
2. X58286; G339754; -...
2. X68286; G339750; -...
2. X75866; G339750; JOII
3. X75864; G339750; JOII
3. X75865; G339750; JOII
3. X75865; G339750; -...
3. X75860; A38910; A38010.
3. X75860; A38010.
3. X75860; A38010.
3. X75860; A38010.
3. X75860; A38010.
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                                                                                                                                                                                                                                                                                        A38208; A38208
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                                                                                                                                                                                                                                                        31-JUL-94.
07-DEC-95.
11-JAN-97.
 JOINED.
                                                                                                                                                                                                 NGFR_1; 3.
NGFR_2; 3.
_DOMAIN; 1.
_GLYCOPROTEIN; REPEAT; S
                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X THER-CYS 1.
THER-CYS 2.
THER-CYS 3.
THER-CYS 3.
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RESULTING CONTROL OF THE PROPERTY OF THE PROPE
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Best Local
Matches 1
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SEQUENCE OF 1-20.
MEDLINE; 81117268.
BIRKEN S., FETHERSTON J., CANFIELD BIRKEN S., CHEM. 256:1816-1823(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGHB_HUMAN STANDARD; PRT; 165 AA. P0123; P01233; P1-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
SEQUENCE
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CARBOHYD
CARBOHYD
                                                                               [6]
PRELIMINARY SEQUENCE OF 21-165.
MEDLINE; 74011267.
CARLSEN R.B., BAHL O.P., SWAMINATHAN
J. BIOL. CHEM. 248:6810-6827(1973).
                                                                                               SEQUENCE OF 21-165.
MEDLINE; 75211304.
MORGAN F.J., BIRKEN S.,
J. BIOL. CHEM. 250:5247
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 84008141. POLICASTRO P., OVI
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 84093590.
TALMADGE K., VAMVAKOPOULOS
NATURE 307:37-40(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 81012134.
FIDDES J.C., GOODMAN H.M.
NATURE 286:684-687(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT).
                                                                                                                                                                                                                                                                                                            BOIME I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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                                                                                                                                                                                                                                                                                            BIOL.
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llarity 99.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                OVITT
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                                                                                                                                                                                                                                                                                                                              C.E.,
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                                                                                               CANFIELD R.E.; -5258(1975).
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                                                                                                                                                                                                                                                                                                                              HOSHINA M.,
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POTENTIAL.
POTENTIAL.
ALSSING (IN REF. 4).
GPAA -> APP (IN REF. 4)
GPAA -> CEOEAOGF CRC32;
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Pred. No. 2.90e-242;
1; Mismatches 0;
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                                                                                                                                                                                                            R.E.,
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Best Local S
Matches 13
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-1- DEVELOPMENTAL STAGE: MADE BY
EMBL; M0117; G180437; -
EMBL; M13504; G463088; -
EMBL; M13505; G463089; -
EMBL; M13505; G463099; -
EMBL; M13503; G463090; -
EMBL; K03189; G180453; JOINED.
EMBL; K03187; G180453; JOINED.
EMBL; K03188; G180453; JOINED.
PDB; 1HCN; 30-SEP-94.
PDB; 1HCN; 30-SEP-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-5
MEDLINE; 8619596
POLICASTRO P.F.
J. BIOL. CHEM.
                                                                                                                                               PROSITE;
HORMONE;
SIGNAL
CHAIN
DISULFID
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CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
NATURE 369:455-461(1994).

-1- FUNCTION: STANULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
-1- FUNCTION: STANULATES THE MAINTENANCE OF PREGNANCY.
-1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUDDON R.W.;
J. BIOL. CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 90094415
SACCUZO BEEBE J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY ASSIGNMENT MEDLINE; 81215630.
MISE T., BAHL O.P.;
                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 92314469
WEISSHAAR G., HIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFIDE BONDS
                                                                                                            CARBOHYD
                                                                                                                     CARBOHYD
                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                K-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLYCOBIOLOGY 1:393-404(1991).
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           169
                           27
                   PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
         PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
                                                                                                                                                                                                                                                             ,09881
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAHL O.
CHEM. 2
                                                                                                                                                                                                                             PS00261; GLYCO_HORMONE_BETA_1; 1. PS00689; GLYCO_HORMONE_BETA_2; 1. GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF 1-5 FROM N.A.
86195987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      94261179.
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EM. 261:5907-5916(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., HIYAMA J.,
                                                                      43 92
44 108
58 110
13 120
13 120
141
147
158
158
17739 MW;
                                            44.08;
larity 100.08;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ę
                                                                                                                                                                                                                                                                                                                                                   PLACENTA.
:: MADE BY THE FIRST TRIMESTER PLACENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RENWICK A.G.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFIDE BONDS
                                           Score 1030;
Pred. No. 8.
0; Mismatc
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                                                                                                                                                                                                             CHORIOGONADOTROPIN BETA CHAIN
                                                                                -> A (IN
FF1D4802
                                            Mismatches
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                                           DB 1;
3.92e-219;
ches 0;
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CRC32;
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                                                              Length 165
                                            Indels
                                           0;
                                           Gaps
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P50555;
01-OCT-1996
       REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT ROMAIN DISULFID CARBOHYD CARBOHYD
                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFR1
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                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE-KIDNEY;
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                                                                                                                                                                                                                                               9994; G1141753; -.
PS00652; TNFR_NGFR_1; 3.
PS50050; TNFR_NGFR_2; 2.
PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                        TRANSMEMBRANE;
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EXTRACELLULAR TUMOR NECROSIS POTENTI

FACTOR RECEPTOR 1. (POTENTIAL).

4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.

TNFR-CYS 3.

DEATH DOMAIN

Y SIMILARITY.

CYTOPLASMIC 4 X TNFR-CYS

(POTENTIAL)

POTENTIAL.

SIMILARITY SIMILARITY SIMILARITY

POTENTIAL

GLYCOPROTEIN;

REPEAT; SIGNAL; APOPTOSIS.

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A SUTER B., PAUL U.H.;

LI GENE 163:263-266(1995).

LI GENE 163:263-266(1995).

C -I- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD

C RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING

C RECRUITS CASPASE-8 FOOTBOLYTIC ACTIVATION WHICH INITIATES THE

C RECRUIT CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE

C PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE

C PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE

C PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

C -I- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO

C HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

PROVIDE A NOWEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

C HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

PROVIDE A NOWEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

C WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING

PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FRADD, THE RECRUITED TO

THERI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

ACTIVATES AT LEAST TWO DISTINGUES AND THE SUBMELUNG CASCADES, APOPTOSIS AND

C NF-KAPPA B SIGNALING (BY SIMILARITY).

C -I- SUMLERITY: CONTAINS A LA-NGFR/THER-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (REL.
01-OCT-1996 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUS SCROFA (PIG).
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96011645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34, CREATED)
34, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
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APOPTOSIS AND
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Best Local
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                                                                                                                                                                                                      HORMONE;
SIGNAL
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PROSITE; PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                                                                                                                              CRAWFORD R.J., TREGEAR G.W., NIALL H.D.; GENE 46:161-169(1986).
                                                                                                                                                                                                                                                   EMBL; M14966; G176573; PIR; A25808; KTBAB.
                                                                                                                                                                                                                                                                                                                                                                                                        PAPIO ANUBIS
EUKARYOTA; MI
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P07434;
01-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGHB_PAPAN
                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA;
  169
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                                                                                                                                                                                                                                                                                               FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS ARE ESSENTIAL FOR THE MAINTENANCE OF PRECHANCY.
SUBUNIT: HEFTEROBINER OF A COMMON ALPHA CHAIN AND A UNIQUE BE CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: PLACENTA.
THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES
TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KONTVCTCHAGFFLRENECVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYMSENLFQCFNCSLCLNGTVHLSCQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KODTICNCHSGFFLRDKECVSC
                                       h 36.6%;
Similarity 81.3%;
113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                               GLYCOPROTEIN;
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461
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                                                                                                Conservative
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80.3%;
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                                                                             17592 MW;
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Pred.
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Pred. No. 4.23e-200;
                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                      VERTEBRATA; TETRAPODA; MAMMALIA;
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                                       Mismatches
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                                               857; DB 1; L
No. 8.42e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                                                                                                                                                                                                                                      UPDATE)
                                                                             CRC32;
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                                                        Length 165;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A.
WONG G.H., CHEN E.Y., GO
WARTI. ACAD. SCI. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNR1_MOUSE STAN
P25118;
01-MAY-1992 (REL. 2
01-MAY-1992 (REL. 2
01-NOV-1997 (REL. 2
           EMBL;
                                                                                                                                                                                                                                                                                                                         GOODWIN R.G., ANDERSON D., JERZY R., DAV COPELAND N.G., JENKINS N.A., SMITH C.A.; MOL. CELL. BIOL. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFR1 OR TNFR-1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
                                                                                                                                                       ROTHE
                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 93156721.
                                                                                                                                                                                               BEBO
                                                                                                                                                                                                                                                                            BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., GRAY P.W., FELDMANN M., FOXWELL B.M.J.; EUR. J. IMMUNOL. 21:1649-1656(1991).
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 91285014.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 91246168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR
                                                                                                                                                                                                              SEQUENCE FROM N.
                                                                                                                                                                                                                                     ROTHE J.G.,
                                                                                                                                                                                                                                              MEDLINE;
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                      MMUNOGENETICS
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                                                                                                                                                                                    INE; 94245292.

B.F., LINTHICUM D.S.;
NOGENETICS 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPPSPSRLLEPAGTPFLPQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSSKDPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLPSPSRLPGPSDTPILPQ
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M60468; G199826;
M59377; G202097;
                                                                                                                                                                                                                                          92039815.
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ICS 34:338-340(1991)
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                                                                                                                                                                                                                                                                                                                                                                         GOEDDEL
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
RECEPTOR 1 PRECURSOR (P60)
                                                                                                                                                                                                                                                                                                                                                                         A., BENNETT G.L., R
D.V.;
88:2830-2834(1991).
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PFIZENMAIER G.R.;

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SULT 6

D TNR1_RAT STANDARL;

C P22934;

T 01-AUG-1991 (REL. 19, CREATED)

DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TN

GN TNER1 OR TNER-1.

OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPOD!

PUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X59238; G53579;
EMBL; X57796; G54849;
EMBL; X57796; G2430733;
EMBL; M76556; G202102;
EMBL; M86067; G202102;
EMBL; M86067; G202102;
EMBL; M76655; G202102;
PIR; A38634; GGMST1
PIR; S10677; S16677.
PIR; S19021; S19021.
HSSP; P19438; ITURR
MGD; MGI:98781; TNER1.
                                                                                                                                                                                                                                                                                                                  TQNTVCNCHAGFFLRESECVPCS 183
                                                                                                                                                                                                                  KONTVCTCHAGFFLRENECVSCA 165
                                                                                                                                                                                                                                                                                 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
                                                                                                                                                                                                                                                                  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
                                                                                                                                                                                                                                                                                                                                                                        101;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00652; TNFR_NGFR_1; : PS50050; TNFR_NGFR_2; : PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEMBRANE;
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82 191
95 195
154
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394
50129 MW;
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; G54849; -.

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; G202102; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                   35.9%;
                                                          CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                     Score 841;
Pred. No. 7.
23; Mismatc
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R -> G (IN
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TNFR-CYS 1.
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CYTOPLASMIC (POTENTIAL).
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TUMOR NECROSIS FACTOR RECEPTOR 1.
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7.59e-172;
tches 19;
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CRC32;
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                                                                                                 (TNF-R1) (P55).
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RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
RECRUITS CASPASE-8 TO THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC PETCHNES CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -!- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF TRADIS
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERPACE THAT INTERPACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
C PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
TOTER COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
C ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
C NETAPPA B SIGNALING (BY SIMILARITY).
C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR CONTAINS A LA-NGER/TNER-TYPE CYSTEINE-RICH REGION.

REMBL. MAG1323. -
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Best Local
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REPEAT
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RECEPTOR;
SIGNAL
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE; 91090841.

HIMMLER A., MAURE-FOGY I., KROENKE M., SCHEURICH P., PFIZE

LANTZ M., OLSSON I., HAUDTMANN R., STRATOWA C., ADOLF G.R.;

DNA CELL BIOL. 9:705-715(1990).

-I- FUNCTION: RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE

-I- FUNCTION: RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                    161
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                                                                                                             83
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B36555; B36555.
                                                                                                                                                            KONTVCTCHAGFFLRENECVSCA
                                                                                    KQNTVCNCHAGFFLSGNECTPCS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P19438;
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Similarity 68.5%;
98; Conservative
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; TRANSMEMBRANE;
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461 AA;
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158
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                                                                                                                                                                                                              Score 809; DB 1; L
Pred. No. 5.98e-164;
21; Mismatches 24:
                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
82F68B08
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TNFR-CYS 1.
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                                                                                                                                                                                                                                                                                                        POTENTIAL.
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DOMAIN DOMAIN REPEAT REPEAT REPEAT

DOMAIN TRANSMEM

RECEPTOR;

DOMAIN
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RESULT TO DE CONTROL OF THE CONTROL OF T

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Query Match Best Local S Matches 10

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CLOSSET J.,
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P01229;
21-JUL-1986
                                                                            DISEASE
SIGNAL
                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01,
01-NOV-1995 (REL. 32,
01-NOV-1995 (REL. 32,
                                                                                                                                            -i- TISSUE SPECIFICITY: PITUITARY.

-I- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH
-CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
EMBL; X00264; E28368; -.
EMBL; X71273; E21454; -.
EMBL; S71273; E21454; -.
EPIR; A01497; UTHUB.
                                                                                                                                                                                                                                                              WEISS J., AXEI
JAMESON J.L.;
                                                                                                                                                                                                                                                                                                          [7].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
                                                                                                                           HSSP; P01233; 1HCN.
MIM; 152780; -.
                                                                                                                                                                                                                                                        NEW
                                                                                                                                                                                                                                                                                                                                     MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                           WEISSHAAR G.,
                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE OF CARBOHYDRATE MEDLINE; 91122088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHOME B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 21-141.
MEDLINE; 76062547.
SAIRAM M.R. LI C.H.;
BIOCHIM. BIOPHYS. ACTA 412:70-81(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 84093590.
TALMADGE K., VAMVAKOPOULOS
NATURE 307:37-40(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE)
                                                                                                                                                                                                                                                                                   MEDLINE; 92085985.
                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                         KEUTMANN H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 73090987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE OF
                                                                                                                                                                                                ENGL. J. MED. 326:179-183(1992).

FUNCTION: PROMOTES SPERMATCOENESIS AND OVULATION BY STIMULF TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                J. BIOCHEM. 195:257-268(1991).
                                                                                                                                                                                                                                                                                                                ENDOCRINOL.
                                                                                             PS00261; GLYCO_HORMONE_BETA_1; 1.
PS00689; GLYCO_HORMONE_BETA_2; 1.
GLYCOPROTEIN; SIGNAL; PSEUDOHERMAPHRODITISM;
                                                                                                                                                                                                                                                                                                                                                                                   91122088
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                                                                                                                                                                                                                                                                           AXELROD
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29:97-100(1973).
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L. 6:904-913
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                           WHITCOMB R.W.,
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3(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.C.,
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        LUTROPIN BETA C
BY SIMILARITY.
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                                                                                                                                                                                                                                                                           HARRIS
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                                                                 CHAIN
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                                                                                                                                                                                                                         A UNIQUE BETA
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01-OCT-1996
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CONFLICT
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EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                    SIMULA A.P., AMATO F., FAAST R., LOPATA A., BERKA J., NORMAN R.J.;
BIOL. REPROD. 53:380-389(1995).
-I- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT BE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
                                                                                                                                                                                                                                                                                                                                                                                    CHORIOGONADOTROPIN BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                           SEQUENCE
                                                                                                                                                                               SIGNAL
                                                                                                                                                                                       HORMONE;
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SIMULA A.P., AMATO F.,
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
  169
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                                                                                                                                                                                                                  CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
TISSUE SPECIFICITY: PLACENTA.
5L; U04447; G606607; -.
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                                     Similarity
90; Conse
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92; Conse
                                                                                                                                                                                       GLYCOPROTEIN;
                                                                                                                                                                                              PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2;
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141
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(REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
                                      Conservative
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CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                              30.3%;
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76
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                                    Score 709; 1
Pred. No. 2.:
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RECEPTOR-BINDING).
E -> Q (IN REF. 2).
MISSING (IN REF. 2).
HPQL -> PQH (IN REF. 2).
W; A2457F6F CRC32;
                                                                                 BY SIMILARITY
CHORIOGONADOTROPIN E
BY SIMILARITY
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Pred. No. 5.55e-147;
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                                                                          E36A4DB3 CRC32;
                                      Mismatches
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                                     DB 1; Le
1.18e-139;
ches 23;
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                                                       Length 164;
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                          P04651;
13-AUG-1987
01-JAN-1988
01-OCT-1996
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HORMONE;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEIGH S.E.A., STEWART F.;

J. MOL. ENDOCRINOL. 4:143-150(1990).

-I- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

EMBL; X80116; G510971; -

EMBL; X80116; G510971; -

EMBL; X53669; E27544; ALT_SEQ.
13-AUG-1987 (REL. 05, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
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EUKARYOTA; METAZOA; CH
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COMBARNOUS
SUBMITTED (JUL-1994) TO E
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EMBL/GENBANK/DDBJ
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Pred. No. 3.88e-120;
21; Mismatches 23;
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BY SIMILARITY.
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J DATA BANKS
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SEQUENCE
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DISULFID
CARBOHYD
                                                        ISHB_HORSE STANDARD; PRT; 169 AA. P08751; P01234; P01234; P01-AUG-1988 (REL. 08, CREATED) O1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE) O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGHUIN-ROGISTER G., HENNEN G.;
EUR. J. BIOCHEM. 39:235-253(1973).
-:- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
EMBL; M11007; G163301; -.
EMBL; M11506; G163299; -.
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BOS TAURUS (BOVINE).
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                  EQUUS CABALLUS (HORSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PERISSODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 85182575. MAURER R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 85207729. VIRGIN J.B., SILVER
SEQUENCE FROM N.A.
                                                LHB
                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A01499; UTBOB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-139. MEDLINE; 74075724.
                                                                                                                                                                                                                                                                                                                                                                                                                                  HORMONE;
                                                                                                                                                    229
                                                                                                                                                                                            169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOL.
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                                                                                                                                                  Similarity 72; Consen
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL;
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                                                                                                                                                                                                                                  26.2%;
larity 64.9%;
Conservative
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43
46
54
58
113
113
112
112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260:4684-4687(1985).
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130
108
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123
126
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Q -> E (IN REF. 3).

P -> S (IN REF. 2).

GP -> PG (IN REF. 3).

Q -> E (IN REF. 3).

W; 82879D1F CRC32;
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Pred. No. 2.94e-116;
22; Mismatches 17;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                          PRECURSOR
                                                                                                                                                                                                                                                       Length 141;
                                                          (LSH-B/CG-B).
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LSHB_SHEEP
P01231;
21-JUL-1986
01-NOV-1995
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DISULFID
DISULFID
DISULFID
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CARBOHYD
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PIR; ;
PIR; ;
PIR; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
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SHERMAN G.B., WOLFE M.W., FARMERIE T.A., CLAY C.M., THREADGILL D.S., SHARP D.C., NILSON J.H.;

MOL. ENDOCRINOL. 6:951-959(1992).

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAMM J.B.L., HARD K., KAMERLING J.P., VLIEGENTHART J.F.G.;
EUR. J. BICCHEM. 189:175-183(1990).
-I- FUNCTION: PROMOTES SPERMATGGENESSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WARD D.N., MOORE W.
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE OF CARBOHYDRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUGINO
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MEDLINE; 87250475.
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MEDLINE: 87250476.
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                                                                                                                             229
                                                                                                                                                                          169
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mes 84; Conser
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RD D.N., MOORE W.T. JR., BURLEIGH B
PROTEIN CHEM. 1:263-280(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USFIELD G.R., LIU W.-K., SUGINO H., BIOL. CHEM. 262:8610-8620(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                     L; S41704; G252741; A01503; KTHOB.; A29304; A29304.; A29305; A29305; A29305.; A41917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, COLLITROPIN AND GONADOTROPIN.
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
PTM: AT LEAST FOUR O-GLYCOSYLATION SITES ARE PRESENT.
L; S41704; G252741; -.
                                                                                                                                                                                   PLCRPINATLAAEKEACPICITETTSICAGYCPSMVRVMPAALPAIPQPVCTYRELRFAS
                                                                                                     QPLTSTSTPTPGAS 157
                                                                                                                                     IRLPGCPPGVDPMVSFPVALSCHCGPCQIKTIDCGVFRDQPLACA-P--QASSSSKDPPS 143
                                                                                                                                                                      PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTWTRVLQGVLPALPQVVCNYRDVRFES
                                                                                -SLPSPS-RLPGPS
                                                                                                                         IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP
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                                                                                                                                                                                                                                                                                                                                                                                          PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2; GLYCOPROTEIN; SIGNAL.
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(REL.
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                                  STANDARD;
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62.7%;
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CREATED)
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BY SIMILARITY.
SEQUENCE UPDATE)
                                                                                                                                                                                                                    Score 613; DB 1; L
Pred. No. 5.13e-116;
22; M1smatches 23;
                                  PRT;
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HORMONE;
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MEDLINE; 73190035.
SAIRAM M.R., SAMY T.S.A.,
                                                                                                                   CARBOHYD
                                                                                                                           MOBI
                                                                                                                                                                            CHAIN
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MEDLINE; 72211145.
LIU W.-K., NAHM H.S., SWEENEY C.M.,
J., BIOL. CHEM. 247:4365-4381(1972).
                                                                                                                                   DISULFID
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LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                       PIR; A01500; UTSHB. PIR; S09232; S09232.
                                                                                                                                                                                                                                                                                                      STRUCTURE OF CARBOHYDRATE.
MEDLINE; 91006170.
                                                                                                                                                                                                                                                                                                                            ARCH. BIOCHEM.
                                                                                                                                                                                                                                                                                                                                                                                                   D'ANGELO-BERNARD G., MOUMNI M., JUTISZ NUCLEIC ACIDS RES. 18:2175-2175(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 90245669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-PITUITARY
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
       27
PLCQPINATLAAEKEACPVCITFTTSICAGYCLSMKRVLPVILPPMPQRVCTYHELRFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                              P., MCNEILLY J.R., CELL. ENDOCRINOL. 9.
                      Similarity
71; Conser
                                                                                                                                                                                          PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2; SIGNAL; GLYCOPROTEIN.
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METAZOA; CHORDATA;
                                                 25.7%;
larity 64.0%;
Conservative
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                                                G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              ., WALLACE R.M., MCNEILLY A.S., 93:157-165(1993).
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153:572-586(1972).
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                                                MISSING (IN SOME MC
Q -> E (IN REE. 1)
L -> P (IN REE. 1)
R -> Q (IN REE. 2)
PM -> PPM (IN REF.
E -> Q (IN REF. 4)
GP -> PG (IN REF. 3)
Q -> E (IN REF. 3)
                    Score 602; DB 1; I
Pred. No. 2.36e-113;
22; Mismatches 18;
                                                                                                                                LUTROPIN BETA C
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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AND 4).
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CARBOHYD
MOD_RES
VARIANT
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EMBL; D00579; G217694; -.

PIR; A03322; UTPGB.

PIR; A48170; A48170.

HSSP; P01233; 1HCN.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE MEDLINE; KATO Y.,
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P01232;
                                                                                                                                                                                                                                                                                                                                                                                                   MOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 91063934.
EZASHI T., HIRAI T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOS
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01-NOV-1990 (REL.
01-OCT-1996 (REL.
                                                                                                                                                                                                                                                                                                                                                       MAGHUIN-ROGISTER G., HENNEN G.;
EUR. J. BIOCHEM. 39:235-253(1973)
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 21-139.
MEDLINE; 74075724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA;
EUTHERIA; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUTROPIN
 229
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                                                                                                                                                                                                                                                                                                                     FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMUL THE TESTES AND OVARIES TO SYMPHESIZE STEROIS AND A UNIQUE SUBUNIT: HETERODIAGE OF A COMMON ALPHA CHAIN AND A UNIQUE CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCROFA (PIG)
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                              IRLPGCPPGVDPTVSFPVALSCHCGPCRLSSSDCGGPRAQPLACDRP
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IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP
                                                                h 25.5%;
Similarity 66.4%;
71; Conservative
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HIRAI T.;
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KEL. 34, T

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1, CREATED)
6, LAST SEQUENCE UPDATE)
4, LAST ANNOTATION UPDATE)
PRECURSOR (LUTEINIZING HORMONE)
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                                                                                                  MW;
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V -> R (

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GP -> PG
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V -> R (IN REF. 3)
S -> I (IN REF. 3)
I -> S (IN REF. 3)
GP -> PG (IN REF.
DAZEF539 CRC32;
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1. No. 2.19e-112;
1. No. 2.4es 17;
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Mismatches
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(EF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     KATO
                                                                                Length 141;
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21-JUL-1986 (REL. C

21-JUL-1986 (REL. C

01-OCT-1996 (REL. 3
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P33088;
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01-OCT-1996
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CARBOHYD
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                                                                                                                                                                                                                                                                                           CHAIN
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EMBL; V01542; G758262; -.
EMBL; J00749; G256176; -.
EMBL; D00576; G220808; -.
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                       PROSITE; PS00261; GLYCO_HORMONE_BETA_1; PROSITE; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                                                                                                                                       PIR; A01498; UTRTB. PIR; S42527; S42527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WISTAR-IMAMICHI; TISSUE-ANTERIOR KATO Y., EZASHI T., HIRAI T., KATO T.; ZOOL. SCI. 7:877-885(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JAMESON L., CHI
J. BIOL. CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY;
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 4-141 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHIN W.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUTROPIN BETA CHAIN PRECURSOR
                                                                                  229
                                                                                                                       169
                                                                                                  87
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THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
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                                                                               VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLPHL 135
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IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 277
                                                                                                                                PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELRFAS 86
                                                                                                                      PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
                                                                                                                                                               Similarity 70; Conser
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L., CHIN W.W., HOLLENBERG A.N.,
CHEM. 259:15474-15480(1984).
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larity 64.2%;
Conservative
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01, LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                 LUTROPIN BETA CHAIN.
BY SIMILARITY.
                                                                                                                                                             Score 597; DB 1; I
Pred. No. 3.82e-112;
23; Mismatches 16;
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(LUTEINIZING HORMONE)
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                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80:4649-4653(1983)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHANG
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                                         118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETRAPODA; MAMMALIA;
                                                                                                                                                               16;
                                                                                                                                                                                  Length 141
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                                                                                                                                                               Indels
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27, 27, 34,

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Search completed: Wed May Job time: 19 secs.
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Best Local Similarity 60.6%;
Matches 66; Conservative
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SEQUENCE.

SEQUENCE.

SEQUENCE.

SARASEV V.S., PANKOV Y.A.;

BIOKHIMIA 50:1972-1986(1985).

FINE TOTAL 50:1972-1986(1985).

FINE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

FINE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, ECLLITROPIN AND GONADOTROPIN.

FOLLITROPIN AND GONADOTROPIN.

PIR; PN0139; PN0139.

HSSP; P01233; 1HCN.

FINE PN01233; 1HCN.

FINE PN01233; 1HCN.

FINE PN01233; 1HCN.

FINE PN01233; 1HCN.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; CETACEA.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUTROPIN BETA CHAIN LHB.
                                                                                                                                                              169
                                                                                                                                                                                                                                                                                                                                 TE; PS00261; GLYCO_HORMONE_BETA_1; 1.
TE; PS002689; GLYCO_HORMONE_BETA_2; FALSE_NEG.
TE; GLYCOPROTEIN.
TE; GLYCOPROTEIN.
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                                                08:53:30 1998
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GONADOTROPIN. 1.26e ONIC GONADOTROPIN 1.76e R NECROSIS FACTOR 1.78e NECROSIS FACTOR 5.05e NIZING HORMONE BE 2.46e CULLAR LUTEINIZING 4.12e NIZING HORMONE BE 3.27e OTROPIN II BETA S 9.70e CULAR LUTEINIZING 5.54e OTROPIN I BETA SUBU 3.27e OTROPIN I BETA SUBU 3.27e OTROPIN BETA CHAIN 5.23e TROPIN BETA SUBU 0.51e TROPIN BETA SUBUN 2.64e TROPIN BETA SUBUN 7.41e TROPIN BETA SUBUN 7.96e TROPIN BETA SUBUN 7.96e	nd is derived by analysis of the total score distribution.  SUMMARIES  Query Query Score Match Length DB ID Description Pred.	sptremb15 1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mam 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_ver 13:sp_unclassified  s: Mean 42.863; Variance 77.650; scale 0.552 d. No. is the number of results predicted by chance to have greater than or equal to the score of the result being	iption: (1307) from US ct Score: 2341 nce: 1 SRTSLLLAFGLLC ng table: PAM 150 Gap 11 hed: 140555 segs, 42 processing: Minimum Match 0 Listing first 4	AA John F. Collins, Biocomputing Research Uni 1993-1997 University of Edinburgh, U.K. ibution rights by Oxford Molecular Ltd rotein database search, using Smith-Waterman 9 6 08:53:48 1998; MasPar time 15.81 Second 817.861 Million cell upd rated.	
894440000000000000000000000000000000000	Pred. No.	tebrate te a printed,		it. algorithm ds	G ‡

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2 1000; 1000; -NOV-1996 -JAN-1998	PRCRI 	1399; 1-NOV-1996 1-NOV-1996 11-NOV-1996 ETA-GONADOT OMO SAPIENS UTHERIA; PR UTHERIA; PR EQUENCE FRO EQUENCE FRO EQUENCE SO ALMADGE K: ATURE 307:3 ATURE 307:3 ATURE 307:3 ATURE 109266 IGNAL. EQUENCE 1	253 253 2248 2248 2248 2214 2214 2214 2214 2210 2210 2210 2210
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≨	KEGCPV KEGCPV KEGCPV SYAVA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	JLREL.  JLREL.  JLREL.  NN).  CHOR  NKOPOUL  984).  1548  1548  43.7  99.3	277 2 426 2 2 348 11 349 11 349 11 355 11 6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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PRT; CREATED) LAST SEQ LAST ANN	TTIC	REAT AST VER VER C., C., AC AC	014866 014865 000276 000275 000275 085407 08998 089118 015962 085302 062327 002764 001764 001765 099956 0014798 0014798 014720 015508 014763 014763 014763 014763
; 1 ED) SEQUE ANNOT	CAGYCPT 	VERTEBRATA;  VERTE	ENTS
; 165 AA. ED) SEQUENCE UPDATE) ANNOTATION UPDATE)	IMTRVLQGVLPALPQVVCNYRDVRFES	ED) SEQUENCE UPDATE) ANNOTATION UPDATE) TEBRATA; TETRAPODA; MAMMALIA; TEDDES J.C.; FIDDES J.C.;	SOLUBLE DEATH RECEPTOR 1.71e LYMPHOCYTE ASSOCIATED 1.72e LYMPHOCYTE ASSOCIATED 1.72e LYMPHOCYTE ASSOCIATED 1.72e HOMOLOG OF VACCINIA VI 8.90e GARCIA-1966 RIGHT NEAR 8.90e FINTROTROPIN BETA SUBUN 5.30e THYROTROPIN BETA SUBUN 5.30e THYROTROPIN BETA SUBUN 5.30e THYROTROPIN BETA SUBUN 5.30e THYROTROPIN BETA FACTOR 3.13e OX40 PRECURSOR (FRAGME 1.29e TRAIL RECEPTOR 3. 1.11e CYTOTOXIC TRAIL RECEPT 2.61e FAS ANTIGEN PRECURSOR 6.39e SOMATOTROPIN PRECURSOR 6.39e SOMATOTROPIN PRECURSOR 6.39e DEATH RECEPTOR 5. 3.38e P53-REGULATED DNA DAMA 3.38e APOPTOSIS INDUCING REC 3.38e APOPTOSIS INDUCING REC 3.38e APOPTOSIS INDUCING REC 3.38e APOPTOSIS INDUCING REC 3.38e
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q95185;
01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
THMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

DUTHIE S., NASIR L., ECKERSALL P.D.;

SUBMITTED (CCT-1996) TO EMBL/GENBANK/DDBJ

EMBL; U72344; G1613880; -.

EROSITE; PS00652; TNFR_NGFR_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω95185
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EMBL; K03183; G180444; -.
EMBL; K0092; G180444; JOINED.
EMBL; K03182; G180444; JOINED.
SEQUENCE 165 AA; 17729 MW; B1CAA0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELIS SILVESTRIS CATUS (CAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
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MEDLINE; 84008141.
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EUTHERIA; PRIMATES
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EUKARYOTA; METAZOA; C
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                                                                                                                                                                                                                                                                                          CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
                                                                                                                                                                                          KCRKEMYQVEISPCTYYRDTYCGCRKNOYRYYWSETHFQCLNCSLCLNGTYQISCKETQN 164
                                                                                                                                                                                                                                                                CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
                                                                      TVCTCHAGFFLRENEC
                                                                                                                    TVCTCHAGFFLRGNEC 180
                                                                                                                                                                        KCRKEMGQVEISSCTVDRDTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 43.7%;
Similarity 99.3%;
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180 AA;
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20399 MW;
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                                                                                                                                                                   /CGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1024; DB 2;
Pred. No. 1.26e-200;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5452A6B2 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATA BANKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲,
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Best Local S
Matches 7
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Best Local Similarity 73.2%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O19102;
O1-JAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
LUTEINIZING HORMONE BETA SUBUNIT (FRACMENT).
CERATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPEUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-PITUITARY GLAND;
SHERMAN G.B., LUND L.A.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ
EMBL; U72659; G2462771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O19102
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SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ
EMBL; U90937; G2290398; -
PROSITE; PS00652; TMFR_NGFR_1; 3.
SEQUENCE 471 AA; 51368 MW; 1D60FF4A CF
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01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PITUITARY GLAND;
MEDLINE; 97449288.
SHERMAN G.B., LUND L.A.,
GENE 195:131-139(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               019131
                                                                                                                                                                                                                                                                                                       SEQUENCE
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       169
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RODTICHCHMGFFLKGAKCISC
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                                                                                                                                                   Similarity 71; Conser
                                                                                                                                                                                                                                                                                                       135 AA;
                                                                                                                                                       Conservative
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                                                                                                                                                                                     25.5%;
                                                                                                                                                                                                                                                                                                   14212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUNICK
                                                                                                                                               Score 596; DB 4; L
Pred. No. 2.46e-103;
20; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
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Pred. No. 5.05e-171;
21; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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1D60FF4A CRC32;
                                                                                                                                                                                                                                                                                                   F4F196D2 CRC32;
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D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WINN R.J.;
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                                                                                                                                                   16;
                                                                                                                                                                                                                       Length
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ID Q62778
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 68; Conser
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01-NOV-1996
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01-NOV-1996 (TREMBLREL. (
01-JAN-1998 (TREMBLREL. (
LUTEINIZING HORMONE BETA
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BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
EMBL; U25653; G915217; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAPUR V., MATZUK M.M.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, U25145; G93045; -.
MGD; MGI:96782; LHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q60844;
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
TESTICULAR LUTEINIZING)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=129 SVEV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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MEDLINE; 95283549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA;
                                                                                                                 229
                                                                                                                                                                                                                               169
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                                                                                                                                                                                                                                                          PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELAFAS 86
                                                                                                              IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP
                                                                                                                                                                                                                         PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
                                                                                                                                                                                                                                                                                                                                          24.98;
larity 62.48;
Conservative
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larity 63.3%;
Conservative
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  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14880 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01, CREATED)
01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
a (LUTENIZING HORMONE BETA-SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 595; DB 10;
Pred. No. 4.12e-103;
24; Mismatches 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                       Score 582; DB 10; Pred. No. 3.27e-100; 24; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
  PRT;
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  140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UPDATE)
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Best Local S
Matches 4
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Best Local :
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Q1-FEB-1997 (TREMBLREL. 02, CREATED)
Q1-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
Q1-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDAT
GONADOTROPIN II BETA SUBUNIT PRECURSOR.
CARASSIUS AURATUS (GOLDPISH).
EUKARYOTA, METAZOA: CHORDATA; VERTEBRATA; PISCES;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
Q91121;
01-NOV-1996
01-NOV-1996
                                                                                                              LT 10
Q91121
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Q63013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHANG F.P., RANNIKKO A., HUHTAN BIOCHEM. BIOPHYS. RES. COMMUN. EMBL. UZ5803; G904026; SEQUENCE 80 AA; 8515 MW; 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAQUE DAWLEY;
MEDLINE; 95283549.
ZHANG F.P., RANNIKKO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
TESTICULAR LUTEINIZING F
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01-NOV-1996
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YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; D88024; G1644243; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                               263
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Local Similarity 50.0%;
les 54; Conserva+4...
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                                                                                                                                                                                                                                                                                                                                                                        MVRVLPAALPPVPQPVCTYRE-RFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRLPDCPPGVDPHITYPVALSCDCSLCTMDTSDCTIESLQPDFCMSQR 134
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                                                                                                                                                                                                                            GGPKDHPLTCDDPRF
                                                                                                                                                                                                                                                                                                                                          MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
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45; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.7%;
[larity 60.0%;
Conservative
(TREMBLREL.
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUHTANIEMI I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
  CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 391; DB 10;
Pred. No. 2.54e-58;
18; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 430; DB 12;
Pred. No. 9.70e-67;
22; Mismatches 32
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GONADOTROPIN II BETA SUBUNIT.
; 7205FD03 CRC32;
                                                                                                              PRT;
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  SEQUENCE UPDATE)
                                                                                                              147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 80
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Best Local s
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Best Local 9
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                                                                                                               013050;
01-JUL-1997
01-JUL-1997
01-JUL-1997
EUKARYOTA; METAZOA; CHORDATA; OSTEICHTHYES; ACTINOPTERYGII; [1]
                                                                01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDAT
GONADOTROPIN I BETA SUBUNIT PRECURSOR.
CYPRINUS CARPIO (COMMON CARP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TSAI H.J., YANG L.T.;
SUBMITTED (JAN-1994) T
EMBL; L11722; G437308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GONADOTROPIN BETA-SUBUNIT.
ACANTHOPAGRUS LATUS.
EUKARYOTA; ANIMALIA; METAZOA;
ACTINOPTERYGII; PERCIFORMES; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q90225;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HASSIN S., ELIZUR A., ZOHAR Y.;
J. MOL. ENDOCRINOL. 15:23-35(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L35096; G598255; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 15.4%;
Similarity 44.5%;
49; Conservative
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33
147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                 PRELIMINARY;
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147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15330 MW; F87577B5 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 353; DB 12;
Pred. No. 3.27e-50
22; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 361; DB 12;
Pred. No. 6.54e-52;
24; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST ANNOTATION UPDATE)
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GONADOTROPIN II BETA SUBUNIT; 292F2F62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHORDATA;
PERCOIDEI;
                          CYPRINIFORMES
                                               VERTEBRATA;
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 36;
                                                                                                                                                                                                                              130
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                                             PISCES; GNATHOSTOMATA;
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                                                                                                             UPDATE)
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ID P79357
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                   Q98848;
01-FEB-1997
01-FEB-1997
01-FEB-1997
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01-MAY-1997
01-MAY-1997
          EMBL; DE
SIGNAL.
                                                                                                                                                                                              LT 14
Q98848
                                                                                      CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA;
OSTEICHTHYES; ACTINOPTERYGII;
                                                                                                                         01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDAT
GONADOTROPIN I BETA SUBUNIT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
                                TISSUE-PITUITARY GLAND;
YOSHIURA Y., KOBAYASHI M
SUBMITTED (OCT-1996) TO
                                                                                                                                                                                                                                                                                                                                                                             KANIA S.A., FRANK L.A., ODOM T.F.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; U89294; G1872550; -
SEQUENCE 138 AA; 15571 MW; 332E4E82 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
THYROTROPIN BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOBAYASHI M., IWASAKI M., KONDO H., YOSHIU
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ
EMBL; AB003583; D1020895; -.
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P79357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-PITUITARY;
                                                                                                                                                                                                                                           218
                                                                                                                                                                                                                                                                                 162 VSCAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQG-V-LP--ALPQV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 CRPINATLAVEKEGCPYCITVNTTICAGYCPTMTRVLQGVLPALP-QVVCNYRDVRFESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 RLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 273
                                                                                                                                                                                                                                                     85 EFKGCPARADSVFTYPVALSCECSKCNSDITDCGALSQQTLSCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 CRITNISITVESEECGSCITIDITACAGLCKTQESVYRSPL-MLSYQNTCNFREWTYETY
                                                                                                                                                                                                                                          VCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC
                      D88023;
                                                                                                                                                                                                                                                                                                                                             Similarity
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19
130 AA;
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larity 41.3%;
Conservative
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                      G1644241;
                                                                                                                                                                                              PRELIMINARY;
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45.7%;
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                                             X
                                 EMBL/GENBANK,
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                                           KATO
                                                                                                                                                                                                                                                                                                                                Score 314; DB 4;
Pred. No. 5.23e-42;
22; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 321; DB 12;
Pred. No. 1.80e-43;
24; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
GONADOTROPIN I BE
; 3D37E6B1 CRC32;
POTENTIAL.
                                                                                         VERTEBRATA; P
CYPRINIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA;
                                                                                                                                                                                              PRT;
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WBANK/DDBJ DATA BANKS
                                 AIDA :
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                                 DATA
                                                                                                  PISCES;
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                                                                                                                                                                                                                                                                                                                                   29;
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                                 BANKS
                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                     BANKS
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                                                                                                  GNATHOSTOMATA;
                                                                                                                                                                                                                                                                                                                                 Indels
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Search completed: Wed May 6 08:55:06 1998 Job time : 78 secs.
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ID Q16163
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Best Local Similarity 45.7%; Pred. No. 2.21e-41;
Matches 48; Conservative 22; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.3%;
Best Local Similarity 40.4%;
Matches 42; Conservative
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O16163;
O1-NOV-1996 (TREMBLREL. O1, CREATED)
O1-NOV-1996 (TREMBLREL. O1, LAST SEQUENCE UPDATE)
O1-NOV-1996 (TREMBLREL. O1, LAST ANNOTATION UPDATE)
THYROID-STIMULATING HORMONE BETA SUBUNIT (FRAGMENT).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE; 94254248.

MIYOSHI I., KASAI N., HAYASHIZAKI Y.;

MIPPON RINSHO 52:940-947(1994).

EMBL; S70587; G546849; -.

NON_TER 138 138
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                                                                                                                                                                               71 VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGKCNTDYSDC 115
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130 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
15627 MW; 0539646F CRC32;
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed May 6 13:40:53 1998; MasPar time 1173.41 Seconds 1494.904 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: Scoring table: >US-08-804-166-5 (1-1147) from US08804166.seq 1147 1 TCGAGATGGCTACAGGTAAG......AATCTTAAGGATCCCTCGAG 1147
AGCTCTACCGATGTCCATTC......TTAGAATTCCTAGGGAGCTC

Nmatch STD : TABLE default Gap 6 Dbase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database: . emb153
1:em\_in 2:em\_or 3:em\_om 4:em\_ov 5:em\_pl 6:em\_htg
7:em\_hum1 8:em\_hum2 9:em\_ba 10:em\_ro 11:em\_un 12:em\_vi
13:em\_pat
genbank105
14:gb\_ro 15:gb\_om 16:gb\_ov 17:gb\_in 18:gb\_pl 19:gb\_ba
20:gb\_st 21:gb\_vi 22:gb\_ph 23:gb\_sy 24:gb\_un 25:gb\_pat
26:gb\_htg 27:gb\_pr1 28:gb\_pr2

Statistics: Mean 11.072; Variance 4.877; scale 2.270

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

7 9 9 11 12 13 14	138481	Result
	55555555555555555555555555555555555555	Score
444. 444. 444. 11. 444. 11. 11.	444. 444. 444. 1	Query Match
2087 2111 2111 2112 2112 2161 2175 2175 2176 6889		Length DB
25 25 25 25 25	225	BB
HUMTNER HUMTNERB A26412 HUMTNERC HSTNER1A I64751 A43873 A19907 I26928	A29103 A29098 HUMTNFRP A21522 I43805	ID
Human tumor necrosis f Homo sapiens tumor nec cDNA for (55kD TNF-BP) Human tumor necrosis f H.sapiens TNF-R mRNA f Sequence 1 from patent Sequence 1 from Patent Synthetic nucleotide s Sequence 2 from patent	H.saplens mRNA for TNF Synthetic DNA for TNF- Human tumor necrosis f TNF alpha gene. Sequence 24 from paten	Description
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252	252	252	252	252	255	255	262	263	287	287	288	288	288	289	301	307	316	345	345	364	364	366	373	375	375	464	467	468	473	499
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MMTNFRE5	MUSTNFX	MMP55R	MUSMTNFR1	MUSTNFR2	143811	A20263	HSGONA	RATTNER	163120	HUMGHN	I41411	HUMGH	HSGROW2	I02855	SSU19994	FCU72344	HUMGHCSA	I43809	A20259	A20253	I43787	A20254	I43786	I43813	A20713	0	52	S	A29099	A20255
Mouse mRNA for 55-kDa	POT N	Murine mRNA for p55 tu	Mouse tumor necrosis f	mor neci	Sequence 53 from paten	tic nucleotide	Human messenger RNA fo	r necrosis f	from pat	owth hormone	Sequence 5 from patent	growth ho	m line gene	from Pat	a p55 TNF	Felis catus tumour nec	owth hor	4	Synthetic nucleotide s	ucleotide	Sequence 3 from patent	c nucleotide	1 from E	6 from pate	nucleot	fron		-	Synthetic DNA for TNF-	r C C
.21e-	.21e-	.21e-	.21e-	.21e-	.77e-	.77e-	.28e-	.84e-	.66e-	.66e-	.72e-	.72e-	.72e-	1.09e-235	.30e-	.40e-	.26e-	.80e-	.80e-	.00e+0		.00e+0				.00e+0	ဇ္		0	0.00e+00

### ALIGNMENTS

RESULT :	A29103	1331 bp	DNA	PAT	03-JUL-1995	
DEFINITION ACCESSION NID KEYWORDS	ens 17	RNA for TNE	-binding po	lypeptide from	mRNA for TNF-binding polypeptide from patent EP0393438.	
SOURCE ORGANISM	human. Homo sapiens	8				
	Eukaryotae; Vertebrata;	mitochondr Eutheria;	rial eukaryo	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chordata; Lnidae; Homo.	
REFERENCE	1 (bases 1	(bases 1 to 1331)				
AUTHORS	Hauptmann, R	., Himmler,	A., Maurer-	Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stratowa, C.	ratowa, C.	
JOURNAL	Patent: EP	0393438-A	Patent: EP 0393438-A 53 24-OCT-1990;	Patent: EP 0393438-A 53 24 -Peteri and was coursy careford Patent: EP 0393438-A 53 24 -Peteri and was course careford Patent Indiana Course Co	d chereror	
FEATURES		Location/Qualifiers	ifiers	1		
		organism="Homo sapie /db_xref="taxon:9606"	organism="Homo sapiens" /db_xref="taxon:9606"			
ORIGIN	290 4	# C	202 6 505	٢		
Query Mat Best Loca Matches	Query Match 44.1%; Best Local Similarity 98.1%; Matches 521; Conservative		Score 506; DB 25; Pred. No. 0.00e+00; 0; Mismatches 9	DB 25; Length 1331; 00e+00; hes 9; Indels 1	1331; ls 1; Gaps 1;	
Db 333 (	SATAGTGTGTGTC	CCCAAGGAAA	TATATCCACCC	GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC	TTTGCTGTACC 392	
Оу 344 (	SATAGTGTGTGTC	CCCAAGGAAA	VTATATCCACCC	GATAGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC	TTGCTGTACC 403	
Db 393 /	AAGTGCCACAAAG	GAACCTACTTO	TACAATGACTG	AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC	AGGATACGGAC 452	
Оу 404 і	NAGTGCCACAAAG	GAACCTACTTO	TACAATGACTG	AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC	AGGATACCGAC 463	
Db 453	IGCAGGGAGTGTG	AGAGCGGCTCC	TTCACCGCTTC	TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC	SACACTGCCTC 512	
Оу 464	CCAGGGAGTGTG	AGAGCGGCTCC	TTCACCGCTTC	TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACCCACCTCAGACACTGCCTC	SACACTGCCTC 523	

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REFERENCE
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                                                                                            TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
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          CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,
TNF-receptor, TNF-binding protein and DNA coding there
Patent: EP 0393438-A 48 24-OCT-1990;
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/db_xref="taxon:32644"
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                                                                                      /product="INF receptor"
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275. .1513
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155. .274
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155. .1516
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/db_xref="taxon:9606"
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Vertebrata; Eutheria
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Location/Qualifiers
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Query Match

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Unknown.
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I43805
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1. 2062
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 2887)
1 (bases - Terria Marcher, F.J., Lee, A.L., Rice, G.C.,
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/db_xref="taxon:9606"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 211)
Loetscher, H., Pan, Y.-C.E., Lahm, H.-W., Gentz, R., Brockhaus, M.,
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/product="tumor necrosis factor receptor"
/db_xref="pID:q339754"
/db_xref="pID:q339754"
/translation="MGLSTYPDLLFPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHGLSC
SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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187. .273
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/db_xref="taxon:9606"
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                                                                                             /gene="TNF receptor"
/note="55 kDa"
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A26412
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l Similarity 98.18;
521; Conservative
                                                              1 (bases 1 to 2111)
Brockhaus, M., Dembic,
Schlaeger, E.J.
         TNF-binding proteins
patent: EP 0417563-A 24 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
LOCATION/Qualifiers
                                                                                                                unidentified unidentified
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                                                                                                                                                                                               cDNA for (55kD TNF-BP)
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PGFTPTLGFSPVPSSTFTSSSTTIPGDCPNFAAPREVAPPYGGADFILATALASDPI
PNPLOKWEDSAHKPGSLDTDDDATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLEIGU
GRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
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/gene="TNF receptor"
274. .1551
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Pred. No. 0.00e+00;
0; Mismatches 9
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                                                              tumor necrosis factor Human cDNA to mRNA. Homo sapiens
                                                                                                                                 cds.
M63121 M75861
            Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Primates; Catarrhini; Hon
1. (bases 1 to 2112)
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//product="55 kD TNF-BP"
//db_xref="910;9904969"
//translation="MGLSTVPDLLLPLYLLELLVGIYPSGVIGLVPHLGDREKRDSVC
//translation="MGLSTVPDLLPLYNDCPGPGQDTDCRECESGSFTASENHLKHCLSC
PQKKYIHPQNNSICCTRCHKGTYLYNDCPGPGQDTDCRECEGGTTVHLSCQE
KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
KQNTVCTCHAGFFLRENECVSCSNCKKSLSCTKLCLPQIENVGGTEDSGTTVLLPLVI
FFGLCLLSLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
PGFTPTLGFSVPVPSSTTTSSSTYTPGDCPNFAAPRRYAPPYGGADPILATALASDPI
PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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187. .1554
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98.1%;
Maurer-Fogy, I., Kroenke, M.,
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                                                TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCCTACCCCAGATTGAG
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Pfizenmaier, K., Lantz, M., Olsson, I., Hauptmann, R., Strat Adolf, G.R.
Adolf, G.R.
Molecular cloning and expression of human and rat tumor factor receptor chain (p60) and its soluble derivative, necrosis factor-binding protein
DNA Cell Biol. 9, 705-715 (1990)
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larity 98.18;
Conservative
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/db_xref="pid:g339756"
/translation="MGLSTVPDLLLPLYLLELLYGIYPSGVIGLYPHLGDREKRDSVC
/translation="MGLSTVPDLLPLYNDCPGPGODTDCRECESGSFTASENHLRHCLSC
PQKKYLHPQNNSICCTRCHKGTYLXNDCPGPGODTDCRECESGSFTASENHLRHCLSC
SKCRKEMGOVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
KQNTVCTCHAGFFLREMECVSCSNCKKSLECTWLCLPQIENWGTEDDSGTTVLLPLYI
FFGLCLLSLLEIGLAWRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKRAPNPSFSFP
PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYGADPILATALASDPI
PNPLCKWEDSAHKPOSLDTDDPATLYAVVENVPPLRWKETVRRLGLSDHEIDRLELQN
PNPLCKWEDSAHKPOSLDTDDPATLYAVVENVPPLRWKETVRRLGLSDHEIDRLELQN
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207. .293
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207. .1574
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Pred. No. 0.00e+00;
0; Mismatches 9
Length 2112;
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496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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                            AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC
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l Similarity 98.18;
521; Conservation
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Soluble forms of tumor necrosis factor receptors (TNF-Rs). The for the type I TNF-R, cloned using amino acid sequence data of the teceptor encodes both the cell surface and a soluble form the receptor EMBO J. 9 (10), 3269-3278 (1990)
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TNF-R gene; tumor necrosis factor receptor
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
l (bases 1 to 2161)
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/note="putative"
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Wallach, D., Brakebusch, C., Varfolomee Molecules influencing the shedding of preparation and their use Patent: US 5665859-A 1 09-SEP-1997;

Location/Qualifiers

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                                                                                                                       AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                             AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
                                                                                                            Patent: EP 0657536-A 1 14-JUN-1995;
YEDA RES & DEV (IL)
Other publication ZA 9407962 951121
Other publication JP 7194376 950801
Other publication AU 7574294 950504
Other publication CA 213872 950413.
Location/Qualifiers
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/translation-"mgLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
PQGKY1HPQNNSICCTKOHKGTYLYNDCPGPPQDTDCRECESGSFTASENHLKHCLSC
SKCRKEMGQVEISSCTVDRDTVCGCKKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVGTEDSGTTVLLPLVI
FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGLEGTTTKPLAPNPSFSP
PGFTPTLGFSVPYSSGTYTSGDCPNFAAPRREVAPPYGGADPILATALASDPI
PRPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
GRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
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/db_xref="taxon:32644"
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Best Local Similarity 98.1%;
Matches 521; Conservative
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                                                            AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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A19907
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YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED LOCATION/Qualifiers
1. 2176
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Wallach, D., Nophar, Y., Kemper, O., Engelmann, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified unidentified
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Pred. No. 0.00e+00;
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                                       CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
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 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 6889)

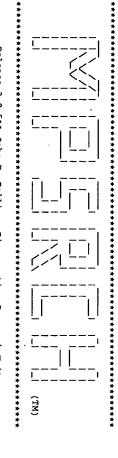
Crowley.C.W.

Method for selecting high-expressing Method for Selecting 2 01-007-1996; Patent: US 5561053-A 2 01-007-1996;
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l Similarity 99.0%;
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Pred. No. 0.00e+00;
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                                                            TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCCTACCCCAGATTGAG 753
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Homo sapiens
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Vertebrata; E
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Location/Qualifiers
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ertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Search completed: Wed May 6 14:00:37 1998 Job time: 1184 secs.

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:19:06 1998; MasPar time 149.10 Seconds 887.730 Million cell updates/sec Tabular output not generated.

Title: >US-08-804-166-5
Description: (1-1147) from US08804166.seq
Perfect Score: 1147
N.A. Sequence: 1 TCGAGATGGCTACAGGTAAG.......

. Sequence: 1 TCGAGATGGCTACAGGTAAG......AATCTTAAGGATCCCTCGAG 1147
Comp: AGCTCTACCGATGTCCATTC.....TTAGAATTCCTAGGGAGCTC

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

nrched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part33 33:part33

Statistics: Mean 9.143; Variance 4.888; scale 1.870

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ا میا اسا				;	Result
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288	3758 3758	504	5000	1006 I	Score 1
30.1	40.8 40.8	43.9	44.1 44.1 44.1	44.1	Query Match
474 2771	2170 608	2175 2141 2176	2062 2088 2111	1334	Query Match Length DB
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Q24442 T76770	Q50870 Q24441	Q90513 Q06285 Q12215	Q24440 Q10883 Q10955	Q06282 Q49932	日
Encodes truncated INF Encodes truncated TNF Rat Fabpl gut-specifi	رى ⊷µ	p55 TNF-R gene. Human Tumour Necrosis Type I TNF receptor.	Encodes TNF -alpha 55k 30kD TNF inhibitor pr Encodes human 55kD TN	m 0 .	Description
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Query Match

44.18;

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Length 1334;

45	44	43	42	41	40	39	38	37	36	35	34	မ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	<u>بر</u> 80	17	16
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		Sequence encoding fis		seque	ncodin	alpha	Bovine alpha subunit	na subu	Porcine alpha subunit	Sequence of gene for	Encodes truncated TNF	0	truncated TN	Single chain gonadotr	ropin	: gly	ed hu	chain	chain	Single chain gonadotr	chain	chain	chain g	chain g	chain	chain g	chain	Human growth hormone	Human growth hormone
.41e-	.40e-	.55e-	.08e-	.03e-	.76e-	.52e-	$\dot{\sim}$	.31e-	.27e-	.08e-	.39e-	.15e-	.15e-	.89e-	ø	.67e-	.67e-	.85e-	.85e-	.85e-	.85e-	.85e-	.85e-	.85e-	.85e-	.85e-	.85e-18	.55e-19	. 82

#### ALIGNMENTS

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RESULT
         DNA encoding TNF binding protein and TNF- receptor - used in the conding TNF binding protein and TNF- receptor - used in the conding TNF binding protein and TNF- receptor - used in the conding TNF binding protein and rechanismsm to TNF action in the conding TNF- protein.

C prinf-ppi5 is one of 30 positives clones in a screened cDNA library from induced TNF-induced fibrosarcoma cells. A TNF-BP had been isolated from the urine of patients with uraemia and probes/primers were constructed from the determined amino acid sequence.

C produce a vector expressing a soluble form of TNF-binding protein, this plasmid was cut with XmmI, amplified by PCR and the amplified DNA cut with Bamil and EcoRI.

C protein cut with Bamil and EcoRI.

C (BRL) cut with Bamil and EcoRI.

C (BRL) cut with the same enzymes to recover pTNF-BP. This was cut with Bamil and EcoRI, and the recovered fragment inserted into pAD-CMYI (Q06283) to give the required plasmid pADTNF-BP.

See also Q06288-Q06285.
                                                                                                                                                                                                                                                                                                            24-OCT-1990.
26-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT.
Hauptmann R, Himmler A, Maurer-Fogy I,
WPI; 90-321987/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert. Tumour necrosis factor binding protein; TNF-BP; TNF-receptor; pTNF-BP15; ss.
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Q06282;
29-JAN-1991 (first entry)
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EP-393438-A.
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26-MAR-1993; U2938.
30-MAR-1992; US-860710.
(IMMY) IMMUNEX CORP.
Smith CA;
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sig_peptide
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Q49932;
29-APR-1994 (fi
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Lambda derived TNF-R CDNA.

Lambda derived TNF-R CDNA.

Human; tumour necrosis factor receptor; TNF-R; interleukin-1 re

II-1R; fusion protein; linker; TNF; II-1; cachexia; cerebral ma

rheumatoid arthritis; diabetes; multiple sclerosis; septic shoc

pulmonary fibrosis; silicosis; allograff; xenograft; rejection;

graft verses host disease; sepsis; inflammation; allergy;
New fusion protein tumour necrosis factor and human in receptor - useful in therapy, diagnosis and assays of rheumatoid arthritis, diabetes, cerebral malaria, seps Disclosure; Page 57-59; 85pp; English.
                                                                                                              W09319777-A.
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Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T;
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larity 98.18;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 506; DB 8;
Pred. No. 0.00e+00;
0; Mismatches 9
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Q20973 standard; DNA; 2062 Q20973; 11-MAY-1992 (first entry) TNF-alpha binding protein g Tumour necrosis factor alph extracellular domain.

alpha; gene

autoimmune

diseases;

Location/Qualifiers 155..1522

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PN GB2246569-A.

PD 05-FEB-1992.

PF 15-JUN-1999; 013410.

PF 15-JUN-1999; GB-013410.

PR 15-JUN-1999; GB-013410.

PR (CHAR-) CHARING CROSS SUNLE.

PI Feldman M, Gray P, Turner M, Brennan F;

PI Feldman M, Gray P, Turner M, Brennan F;

PR WPI; 92-043613/06.

PR P-SDB; R20787.

PR WPI; 92-043613/06.

Pr - useful in treating cachexia, sepsis and auto immune diseases

PT - useful in treating that of DNA encoding tumour necrosis factor alpha

CC The sequence is that of DNA encoding tumour necrosis factor alpha

CC in lambda gtil using a probe (020974). The DNA also encodes the

CC extracellular domain of human TNF alpha receptor and as such it is

CC useful for treating diseases where TNF alpha is involved as a

CC causative agent, e.g. cachexia, sepsis and autoimmune diseases,

CC specifically rheumatoid arthritis. See also Q20974.

Cachennece 2062 BP; 429 A; 616 C; 573 G; 444 T;
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Best Local
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/*tag= b
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/*tag= c
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Local Similarity 98.1%;
local Similarity 98.1%;
les 521; Conservative
                                                                                                     ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                             gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc
               tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag
                                                                                                                                                                                                                          cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt
                                                                                                                                                                                                                                                                               agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac
                                                                                                                                                                                                                                                                                                                                    tgcagggagtgtgagagcggctccttcaccgcttcagaaaaaccacctcagacactgcctc
                                                                                                                                                                                                                                                                                                                                                                                          amgtgccacamaggmacctacttgtmcamtgactgtccmggcccggggcaggmtmcggmc 394
                                                                                                                                                                                                                                                                                                                                                                                                                               GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403
                                                                                                                                                                                                                                                                   AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
                                                                                                                                                                                                                                                                                                                      TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                                                                                                                                                                                                                                                                                                                                           AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 506; DB 3;
Pred. No. 0.00e+00;
0; Mismatches 9
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Claim 4; Fig 1; 43pp; English.

This sequence encodes human TNF-alpha 55kD receptor. A placenta cDNA library in gtil was screened with probe 029236. Ten hybridising clones were plaque purified and cDNA size determined by PAGE against an Eco RI digested phage DNA. The inserts of two cDNA clones were then sequenced. The coding region of the majority of the human TNF-alpha 55kD receptor was isolated as an EcoRI fragment encoding 374 amino acids, and cloned into a mammalian cell expression vector, resulting in pTTNFR. A derivative of the TNF-alpha receptor was produced by engineering a termination codon just prior to the transmembrane domain. PCR with primers 029237,8 generated a 300bp restriction fragment which was cloned into pTTNFR, giving pTNFRecd. DNA sequencing confirmed this contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected into monkey COS-7 cells.
                                                                                                                                                                          Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-1991; GO1826.

18-OCT-1990; GB-022648.

(CHAR-) CHARING CROSS SU

Brennan FM, Feldmann M,

WPI; 92-167156/20.
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/product= hu
mat_peptide
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024440;
05-NOV-1992 (first entry)
Encodes TNF-alpha 55kD receptor.
tumour necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
malaria; viral meningits; graft versus host disease;
autoimmune disease; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.
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/*tag= f
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/codon= Seq:"GAC", aa:Asn
-1~ mentide 156..274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9207076-A
30-APR-1992
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mat_peptide 1258..1260
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nat_peptide 1433..1435
 464
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                                                                        aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac
 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
                                                          AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC
                                                                                                                                                                           521;
                                                                                                                                                                          h 44.1%;
Similarity 98.1%;
521; Conservative
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1265..1267
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M, Gray PW, Turner
                                                                                                                                                                        Score 506; 1
Pred. No. 0.1
0; Mismatc
                                                                                                                                                                                                                                    R24080-84,
A; 618 C;
                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                    R27585, Q29236-8
; 572 G; 44:
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                                                                                                         Query Match
Best Local Similarity
Matches 521; Conse
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16-JUL-1990; 058976.

18-JUL-1989; US-381080.

11-DEC-1989; US-450329.

07-FEB-1990; US-479661.

(SYNE-) SYNERGEN INC.

WPI; 91-073847/11.
                                                                                                                                                                                                                                                                                                                                                              13-MAY-1991
30kD TNF inh
Tumour necro
                                                                                                                                                                 Tumour necrosis factor inhibitor - for suppression of TNF-alpha and -beta, useful as therapeutic agent.

Disclosure; Fig 21; 142pp; English.

The sequence encodes the entire 30 kD TNF inhibitor. The clone from which the sequence was obtd. was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA. The whole gene can be inserted into expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and degenerative
                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                         Q10883 standard;
Q10883;
                                                                                                                                            See also Q10878, Q10884 and Q10907.
Sequence 2088 BP; 439 A; 626
                                                                                                                                                                                                                                             P-PSDB; R10986.
                                                    349
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                                                                    TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACACCTGCCTC
        tgcagggagtgtgagagoggctccttcaccgcttcagaaaaccacctcagacactgcctc 468
                                                                                                                                                                                                                                                                                                                                                      sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG
                                                                                                                                                                                                                                                                                                                                                          Nr inhibitor precursor gene in lambda-gt10-7ctnfbp.
necrosis factor; inhibitor; ss.
moiene
                                                                                                        44.18;
llarity 98.18;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 171..1536
                                                                                                                                                                                                                                                                                                                                                                                                 CDNA;
                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                 2088
                                                                                                       Score 506; DB 2;
Pred. No. 0.00e+00;
0; Mismatches 9
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                                                                                                                         Length 2088;
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                                                                                                         Indels
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Best Loc
Matches
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31-AUG-1990; 116707.
31-AUG-1999; CH-003319.
12-SEP-1999; CH-000746.
08-MAR-1990; CH-0001347.
4 200-APR-1990; CH-001347.
A (HOFF) HOFFMANN-LA ROCH
                                                                                                                              prodn.
Claim 4; Fig 1; 26pp; German.
Claim 4; Fig 1; 26pp; German.
Partial amino acid sequences were determined for the 55 and 75kD
Partial amino acid sequences were determined primers were
synthesised based on these partial sequences. The primers were used
to produce a cDNA fragment for use as aprobe to screen a human
placental CDNA bank constructed in lambda gtll. Positive clones were
identified and sequenced. DNA constructs comprising the TNF-BP coding
sequence may also contain a fragment encoding a human Ig domain.
Recombinant constructs are used to transform cells to confer
                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_pepti
/*tag= k
                                                                                                improved TNF-binding
See also Q10956.
Sequence 2111 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAY-1991 (first entry)
Encodes human 55kD TNF-binding protein.
Tumour Necrosis Factor; binding proteins; septic
autoimmune glomerulonephrilis; lymphokine; cytoki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q10955
                                                                                                                                                                                                                                                                                                         Brockhaus M,
Schlaeger EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
/*tag= a
                                                                                                                                                                                                                                                         Insoluble tumour necrosis factor binding proteins encoding them, useful in pharmaceutical prods. and
                                                                                                                                                                                                                                                                                 WPI; 91-081851/12.
P-PSDB; R11082.
                                                                                                                                                                                                                                                                                                                                                                                                          /product= 55kD
EP-417563-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q10955;
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   344
                         307
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larity 98.18;
Conservative
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Pred. No. 0.00e+00;
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PT New protesse capable of cleaving soluble tumour necrosis factor PT (TNF) receptor - from cell-bound TNF- receptor, useful for PT antagonising deleterious effects of TNF.

PS Disclosure; Fig 1; 40pp; English.

CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.

CC Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell CC type. The only region of the receptor whose structure affects the shedding response is the spacer region (see R75012) in the extracellular commain. This region is located close to a site of cleavage of the colecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras CC between human p55 TNF-R and murine epidermal growth factor receptor CC (EGF-R) that are represented by R75007-11. This spacer region was subjected to deletion mutations (R75013-25) and substitutions
                                                                                                                                                                                                                 12-OCT-1993; IL-107268.
(YEDA) YEDA RES & DEV CO L
Batkin M, Brakebusch C, V
WPI; 95-194342/26.
P-PSDB; R75084.
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/product= ps
misc_signal
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Q90513;
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p55; tumour nec
                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermal growth f phorbol myristate
                                                                                                                                                                                                                                                                                                              /note- "possible poly-A signal"
AU9475742-A.
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Best Local :
                   24-OCT-1990.
06-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1989; DE-920382.
(BOEH ) BOEHRINGER INGEL
                                                                                                                                      /*tag= a
/label=huTNF-R
EP-393438-A.
                                                                                                                                                                                                                                                                  ONCASS standard; DNA; 2141 BP.
Q06285;
Q9-JAN-1991 (first entry)
Human Tumour Necrosis Factor-Receptor cDNA insert.
Tumour necrosis factor binding protein; TNF-BP; TN
lambdaTNF-R2; raTNF-R8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (R75026-47). Of the spacer region, the most important residues are Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most important of these. The shedding of the receptor is independent of the side chain identity of these residues, with the exception of a limited dependence on the identity of Val 173. Mutations which alter the conformation of the protein adversely effect the shedding process. The mutations shown in R75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TMP-R from the cell bound TMF-R. Fragments of these inhibitors can be seen in R75017-9, R75033-5 and R75042-3. These protease inhibitors can be used for enhancing TMF function.
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Similarity 98.18;
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Pred. No. 0.00e+00;
0; Mismatches 9
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/product= ty
sig_peptide
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mat_peptide
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misc_RNA
/*tag= d
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raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.

LambdaTNF-R2 encodes the complete human TNF-R2 and was used to construct a plasmid (pADTNF-R) expressing the product the same as pADTNF-BP (see Q06282).

See also Q06282-Q06285.

Sequence 2141 BP; 455 A; 633 C; 593 G; 460 T;
                                                                                                                                          Type I TNF receptor.
Tumour Necrosis Factor; TNF; binding
                                                                                                                                                                           Q12215 standard;
Q12215;
                                                                                            /note= "in-frame
                                                                                                               terminator
                                                                                                                                 Homo sapiens
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larity 97.9%;
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                                                                                                              Location/Qualifiers 244..246
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13-DEC-1989; IL-092697.
12-JUL-1990; IL-095064.
(YEDA ) YEDA RES & DEV CO LTD.
Wallach D, Nophar Y, Kemper C.
Aderts C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant tumour necrosis factor binding protein I - prepd. by transfecting eukaryotic cells with vector contg. deoxyribonucleic acid encoding human type T TNF receptor or soluble domain Disclosure; Fig 1(D); 30pp; English.

The Tumour Necrosis Factor Binding Protein I is the soluble form c type I TNF-receptor and constitutes a fragment of the cell surface form of this receptor, corresp. to its extracellular domain. There is no characteristic poly(A) addition signal near the 3' end of the cDNA. The sequence ACTAAA (tag m) may serve as an alternative to this signal, but with low efficiency. See also Q12212-15.
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/*tag= j
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/note= "may be 2 codons shorter
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Pred. No. 0.00e+00;
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WPI: 96-129407/13.

RWPI: 96-129407/13.

Improved process for the selection of recombinant host cells promoved process for the selection of recombinant host cells process for the selection of recombinant host cells conty. A DNA construct comprising a selectable gene cells conty. A DNA construct comprising a selectable gene process from the cytomegalovirus immediate-early gene, a cells conty region conty. A dicistronic vector (T19930) comprises a regulatory region contyped from the cytomegalovirus immediate-early gene, a celectable dihydrofolate reductase gene positioned within an control having a 5' wild-type ras splice donor site, a downstream control having a 5' wild-type ras splice donor site, a downstream control having a 5' wild-type ras splice donor site, a downstream control having a 5' wild-type ras splice donor and control for the control for an immunoadhesin, Therigg, capable of binding control necrosis factor, and a poly-A sequence. Transfection of CHO CC Unfor cells in nutrient-rich medium gave Therigg in yields of 9.5 cu yml (15-fold higher compared to conventional vector amplified
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Best Local S
Matches 50
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T15931
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Recombinant host cell; dihydrofolate reductase; selectable marker;
DHFR; ras splice donor; dicistronic vector; gene expression;
immunoadhesin; Therigg; tumour necrosis factor; ds.
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28-JUL-1995; U09576.
05-AUG-1994; US-286740.
(GETH ) GENENTECH INC.
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Matches 51
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Claim 2; Figure 1; 17pp; English.

Modification of the tumour necrosis factor receptor by mutation deletion modulates signal transduction and/or cleavage effected the receptor. This modulation of activity can also be achieved using effector proteins which interact with the TNF receptor.

Molecules which interact with the TNF receptor or the effector proteins can be used to treat or prevent diseases associated with the TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft rejection; graft vs. host disease or septic shock. They can also be used to treat overdoses of exogenous TNF.

Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O50870 standard; DNA; 2170 BP.
O50870;
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EP-568925-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating activity of tumour necrosis factor receptor - using peptide(s), antibodies, etc. which interact with critical regions of receptor or effector protein, for controlling auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & Brakebusch C, Wal WPI; 93-353057/45.
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29-APR-1993;
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Q24441;
Q5-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the designed TNF-alpha 55kD receptor derivative, as present in pTNFRecd. This was produced as described 024441. This derivative lacks the 81 carboxyl terminal residues of the cytoplasmic domain. The derivative could be used in the regulation of TNF-alpha mediated responses by binding and sequestering human TNF-alpha e.g. in the treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-1991; G01826.
18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS SUNLEY Brennan FM, Feldmann M, Gray WPI; 92-167156/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1992 (first entry)
Encodes truncated TNF-alpha, 55kD receptor (197 amino acids).
Encodes truncated TNF-alpha, extracellular binding domain;
tumour necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection;
malaria; viral meningits; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide capable of binding human TNF alpha - comprifirst three cysteine-rich subdomains of TNF alpha receptor treating autoimmune disease, septic shock, HIV etc. Example: Fig 7: 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                  See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
Sequence 608 BP; 148 A; 159 C; 165 G; 136
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                                                                                                     aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac
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tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc
                                                                           AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGTTAAGGGCACTGAGGACTCAGGCACCACCAGGTGCTGCCCCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             versus host disease and autoimmune diseases,
                                                                                                                                                                                                                                                                                 l Similarity
474; Conser
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                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                           40.8%;
98.8%;
                                                                                                                                                                                                                                                                                                      Score 468; DB 4;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                     PT New polyceptide capable of binding human TNF alpha - comprises
profirst three cysteine-rich subdomains of TNF alpha receptor for
profirst three cysteine-rich subdomains of TNF alpha receptor for
profirst three cysteine-rich subdomains of TNF alpha receptor
profirst sequence encodes the designed TNF-alpha 55kD receptor
This sequence encodes the designed TNF-alpha 5kD receptor
Cloning of the BgliI/HindIII digested product of a pcR using
Cloning of the BgliI/HindIII digested product of a pcR using
Cloning of the BgliI/HindIII 5'-deltaCla. This introduced
Ca termination codon after amino acid 167, to yield pdeltaIV.
CT his derivative lacks the membrane proximal 4th subdomain, yet
CT retains the ability to bind TNF-alpha with high affinity
C (lopower8 - lopower9 Mpower-1) The deriv. can be used in the
C regulation of TNF-alpha mediated responses by binding and
C sequestering human TNF-alpha e.g. in the treatment of pulmonary
C diseases, septic shock, HIV infection, malaria, viral meningitis,
C graft versus host disease and autolmmune diseases, esp. rheumatoid
C sequence 5,00 APA.
C Sequ
                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q24445;
Q24445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1992 (first entry)
Encodes truncated TNF-alpha 55kD receptor (165 amino acids).
Encodes truncated TNF-alpha; extracellular binding domain;
truncur necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection;
malaria; viral meningits; graft versus host disease;
autoimmune disease; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-0CT-1991; G01826.

18-0CT-1990; GB-022648.

(CHAR-) CHARING CROSS SUNLEY

Brennan FM, Feldmann M, Gray

WPI; 92-167156/20.
                                                                                                                                                                                                                                                                         Sequence
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WO9207076-A.
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                       181 aagtgocacaaaggaacctacttgtacaatgactgtccagggccgggggcaggatacggac
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  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC
                                                                                         GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
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                                                                                                                                                                                l Similarity
379; Conser
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                                                                                                                                                                                                                                                                           504 BP;
                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                       32.7%;
99.0%;
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M, Gray PW, Turner MJC;
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                                                                                                                                                                             Score 375; DB 4; I
Pred. No. 1.89e-267;
0; Mismatches 4;
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                                                                                                                                                                                                                            Length 504;
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                                                                                                                                                                                                                                                                          treating autoimmune disease, septic shock, HIV etc.

Example: Fig 8: 43pp: English.

This sequence encodes the designed TNF-alpha 55kD receptor derivative, as present in pdeltaI. This construct was generated by joining PCR fragments by means of overlaps introduced into the primers used for PCR. Gel purified products of PCR's using 5'Cla, IA, IB, and 5D primers were mixed and subjected to further amplification using 5'Cla and 5D as primers. The resulting fragment was digested with ClaI and BgIII and cloned into ClaI/BgIII digested pTNFRecd, to yield pdeltaI, containing the sequence given. This derivative could be used to regulate TNF-alpha mediated responses by binding and sequestering human TNF-alpha e.g. in the treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis, graft versus host disease and autoimmune diseases, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1992.
18-OCT-1991; G01826.
18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS SUI
Brennan FM, Feldmann M, (WPI; 92-167156/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1992 (first entry)
Encodes truncated TNF-alpha 55kD receptor (155 amino acids).
tumour necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection; implaina; viral meningitis; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide capable of binding human TNF alpha - comprifirst three cysteine-rich subdomains of TNF alpha receptor treating autoimmune disease, septic shock, HIV etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       024442
                                                                                                                                                                                                                                                              See also Q24440-51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R24081.
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gacaccgtgtgtgggctgcaggaagaaccagtaccggcattattggagtgaaaaccttttc
                                                tgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttcttgcacagtggaccgg
                                                                                                                 AGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                               Similarity
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                               R24000, R24080-84,
110 A; 126 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUNLEY RES CENT.
4, Gray PW, Turner
                                                                                                                                                                            Score 345; DB 4; I
Pred. No. 1.16e-243;
0; Mismatches 6:
                                                                                                                                                                                                                                               R27585, Q29236-8
132 G; 106
                                                                                                                                                                                                            Length 474
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises
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RESULT 15
ID T76770;
AC Human GG
KW GDP-L-f
KW alpha liv
KW alpha liv
KW alpha liv
KW acrbohy
KW GDF-L-f
KW GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
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                                   Example 2; Columns 25-28; 24pp; English.

A claimed transgenic mouse expresses, in its intestinal epithelial cells, the enzyme human GDP-1-fucose:beta-D-galactoside 2-alpha-1-cells, the enzyme human GDP-1-fucose:beta-D-yalactoside 2-alpha-1-cells, the enzyme (also called alpha 1, 2 FT) or human GDP-1-fucose: beta-D-N-acetylglucosamide 3/4-alpha-1-fucosyltransferase (also called alpha 1, 3/4 FT). The enzyme is expressed under the control of a gut epithelial cell-specific promoter and Helicobacter pylori adheres to the transgenic cells. The transgenic mouse and intestinal epithelial cells from it are useful as models for screening compounds for the ability to inhibit adhesion of H. pylori to gut epithelial cells. The first 617 nucleotides of the present chimeric sequence encode the promoter from rat liver fatty acid binding protein (Fabpl) which can direct foreign gene expression to the pit cell lineage of the mouse gastric epithelium, to proliferating and non-proliferating cells in intestinal crypts, as well as to the four principal differentiated cell lineages along the crypt-to-villus axis of the small intestine. The remainder of the chimeric sequence corresponds to exon 1 of the human growth hormone (hGH) gene, into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1997 (first entry)

15-SEP-1997 (first entry)

Rat Fabpl gut-specific promoter and human growth hormone exon 1.

Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;

GDP-L-fucose:beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase;

alpha 1, 2 FT; alpha 1, 3/4 FT; tissue-specific promoter;

rat liver fatty acid binding protein; transgene; transgenic mouse;

animal model; intestinal adhesion; Helicobacter pylori infection;

stomach; small intestine; gut; epithelial cell; surface receptor;

carbohydrate antigen; gastritis; peptic ulcer; neoplasia;

gastric adenocarcinoma; Lewis antigen; fucosylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-258275/23.

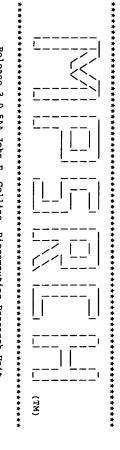
Animal model for Helicobacter pylori infection - comprising Animal model for Helicobacter pylori infection - comprising Animal model for Helicobacter pylori infection - comprising Animal model for Helicobacter pylori infection - comprising Animal model for Helicobacter pylori infection - comprising Animal model for Helicobacter pylori infection - comprising Animal Marketine - comprising Animal model for Helicobacter pylori infection - comprising Animal Marketine                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number= 1
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/note= "Corresponds to nucleotides +3 to
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the rat liver fatty
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(UNIW ) UNIV WASHINGTON
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124-A.
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                                                                                                                                                                                                                                                               Query Match 25.1%; Score 288; DB 31; Length 2771; Best Local Similarity 95.6%; Pred. No. 1.27e-198; Matches 323; Conservative 0; Mismatches 11; Indels 4
                                                                                                                                                                                                                                                                                                        inserted. No hGH will be produced because the initiator Met codon and the first translation stop codon will be from the hFT sequence and there is no ribosome re-entry sequence. The hGH exon 1 ensures efficient splicing of the transgene primary transcript, improves stability of the cytoplasmic hFT mRNA and allows transgene expression to be monitored by in situ hybridisation using a digoxigenin-labelled hGH oligonucleotide.

Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T;
                                                                916
                                                                                                                                                                                                                   306
                      976
                                         126
                                                                                                                                                        798
                                                                                                                                                                                                 740
                                                                                                                                                                        tatcgccatgtaagcccagtatg-gcc-aatctcagaaagctcctggtccctggagggat 855
Indels 4;
                                                                                                                                                                                                                                                                Gaps
```

Search completed: Wed May 6 14:21:41 1998 Job time: 155 secs.



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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:00:59 1998; MasPar time 1055.78 Seconds 1320.756 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: N.A. Sequence: Title: >US-08-804-166-5 (1-1147) from US08804166.seq 1147

Comp: 1 TCGAGATGGCTACAGGTAAG......AATCTTAAGGATCCCTCGAG 1147
AGCTCTACCGATGTCCATTC......TTAGAATTCCTAGGGAGCTC

Scoring table: TABLE default Gap 6

Nmatch

STD :

Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

embl-est

Database:

1:em\_est1 2:em\_est2 3:em\_est3 4:em\_est4 5:em\_est5 6:em\_est6 7:em\_est8 8:em\_gss 9:em\_est13

genbank-est
10:gb\_est1 11:gb\_est2 12:gb\_est3 13:gb\_est4 14:gb\_est5
15:gb\_est6 16:gb\_est7 17:gb\_est8 18:gb\_est9 19:gb\_est10
20:gb\_est11 21:gb\_sts 22:gb\_gss 23:gb\_est12 24:gb\_est13
25:gb\_est14 26:gb\_est15 27:gb\_est16 28:gb\_est17
29:gb\_est18 30:gb\_est19 31:gb\_est20

Statistics: Mean 11.165; Variance 1.901; scale 5.873

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	. 🛪
22 23 33 34 44 111 112 13	Result No.
22222222222222222222222222222222222222	Score
222.88 223.88 223.88 223.7 223.7 211.81	Query Match
34444444 4459 4459 4459 459 459 459 459 4	Length DB
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# ALIGNMENTS

	COMMENT	AUTHORS TITLE JOURNAL	TITLE JOURNAL REFERENCE	REFERENCE AUTHORS	ORGANISM	ACCESSION NID KEYWORDS SOURCE	RESULT 1 LOCUS DEFINITION
Tsutomu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co., Ltd 463-10 kagasuno Kawauchi-cho Tokushima, Tokushima 771-01 Japan Phone: 0886-65-2888	Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:10886-55-2888, Fax:0886-37-1035) Submitted (30-May-1995) to DDBJ by:	_		Homo.  1 (bases 1 to 373)  1 (bases 1 to 373)  Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Fujiwara,T., Takaichi,K., Shimizu,F., Shimada,Y., Shinomiya,H Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hira			μ.
	al 771-01,	Tsutomu		Nagata,M., ', 1,Y.,	idae;	o a polya+	96

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGTTATTATCACAAATCTTAA 308
                                                                                                                                                               Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                         Otsuka cDNA project Unpublished (1996) 2 (bases 1 to 379)
                                                                                                                                                                                                                                                                            Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kug
Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shima
Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Maekawa,H., Nakamura,Y. and Takahashi,E.
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                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="559D08"
                                                                              /tissue_type="placenta"
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                                                                                                                                       High quality sequence stops: 328
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
1. 392
                                                                                                                                                                                                                                                                                                                      WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-Merck EST Unpublished (1995)
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Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
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/clone="144753"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yj31h01.r1 Ho
GLYCOPROTEIN
H00861
                                                                       High qality sequence stops: 344
Source: IMAGE Consortium, LLML free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                     Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                             Hillier,L., Clark,N., Dubuque,T., Elliston,K., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennor Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Trevaskis,E., Waterston,R., Williamson,A., Woh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262;
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Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                           TCAGTGCATGGGCTGCTGCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 158
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                                                                                            TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933
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Otsuka cDNA project Unpublished (1996)

Otheres 1 to 464)
                                                                                                                                                                                                                                                                                                                                                       Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Kaggasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-55-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 262; Conservative
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TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCCAATACT 933
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Tel: 314 286 1800
Fax: 314 286 1810
Email: estar.
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EST.
                                                                                                                                                                                                                                                                 High quality sequence stops: 386
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
1. 467
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
WashU-Merck EST Project
Washington University Sc
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1. (bases 1 to 467)
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/clone="142757"
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                              62 TACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 121
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TACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA
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                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 334
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                           WashIngton University School of Medicine WashIngton University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
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1 (bases 1 to 433)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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larity 98.9%;
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/clone="132966"
104 c 90 g 12
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Best Local Similarity 100.0%;
Matches 260; Conservative
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                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichi Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theri Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 452)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                  WashU-Merck EST ublished (1995)
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/clone="150241"
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TATTATCACAAATCTTAA
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                                                                 GTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGT 240
                                                                                                                          TTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGG 180
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EST; EST(
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Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutica. Co.,Ltd; 463-10 Kayasuno Kawauchi-cho, Tokushima, Tokushima Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takatchi,A., Takeda,S., Watanabe,T., Maekawa,H., Nakamura,Y. and Takahashi,E.
                                                                                                                                                                                                                                                                                                  258;
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/db_xref="taxon:9606"
/clone="539G04"
/tissue_type="placenta"
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Pred. No. 0.00e+00;
0; Mismatches 0
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heria; Primates; Catarrhini; Ho
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                                                                                                                                                                                                                                                                                                                                                        TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993
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                                                                                                                                                                                                                                       CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113
                                                                                                                                                                                                                                                                                                GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053
                                                                                                                                                                               TTGTTATTATCACAAATCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Direct Submission

Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)

Location/Qualifiers
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GLYCOPROTEIN
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C18403
    human clone=145077 (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Otsuka cDNA project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T., Maekawa,H., Nakamura,Y. and Takahashi,E.
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.2%;
llarity 99.6%;
Conservative
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/db_xref="taxon:9606"
/clone="561H02"
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87 c 73 g
                                                                           Homo sapien
IN HORMONES
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                                                                           sapiens cDNA clone 145077 5'
RMONES ALPHA CHAIN PRECURSOR (
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library=Soares placenta Nb2HP vector-pT7T3D modified polylinker host=DH10B (ampicillin
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Pred. No. 0.00e+00;
0; Mismatches 0
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Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops:
Source: IMAGE Consortium, LLi
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
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Unpublished (1995)
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Similarity 100.0%;
254; Conservative
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/clone="145077"
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                                                     Homo sapiens cDNA clone 151651 5' similar to gb:V00518 IN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                   CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGGAGAACCACACGGGCGTGCCACTGCAGT
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                      Human placenta o
D79076
g1180949
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High qality sequence stops: 301
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 482)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ost
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Sarcopterygii; Choanata; Tetrapoda; Miniota; Mominidae; Homen dans Homen da
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The WashU-Merck EST Project
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/clone="151651"
106 c 118 g 14
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"ANNA

J. VILLI.S1 Soares fetal liver spleen la clone 453381 3' similar to gb:V00518 GL CHAIN PRECURSOR (HUMAN);.

N AA779136 g2838467
                                                                                                                                                                                                                                                                                 TTGTTATTATCACAA
                                                                                                                                                                                                                                                                                                                                                       CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                CAGGGTCACAGTAATGGGGGGTTTCATAGTGGGGACCCACACGGCGTGCCACTGCAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGTGCATGGGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (7-Nov-1995) to DDBJ
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical CO.,Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Naga' Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takada,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
Large-scale sequencing project at Otsuka GEN Research Institunpublished (1995)
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463-10 Kagasuno Kawauchi-cho
Tokushima, Tokushima
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Vertebrata; Mammalia;
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Homo sapiens placenta cDNA to mRNA, clone_lib:human placenta
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771-01
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/db_xref="taxon:9606"
/clone_lib="human placenta polyA+"
/closue_type="placenta"
/tissue_type="placenta"
89 c 78 g 93 t
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895
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               CTG-AGCGTG-ATTCTGGGGAATCTG 516
                                                                                  GAAGCAGCCCATGCACTGAAGTAGTGGGGCACCGGGCTCGTAGAAGAATGGGGTTTTC 492
                                                                                                                              GACGTTCTTTTGGACCAACATCGTCTTCTTGGACCTTAGTGGAGTGGGATATGCTCTAGA
                                                                                                                                                GACGTTCTTTTGGACCAACATCGTCTTCTTGGACCTTAGTGGAGTGGGATATGCTCTAGA 432
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CTGTAGCGTGCATTCTGGGCAACCTG
                                                             GAAGCAGCCCATGCACTGAAGTATTGGGGCACCCGGCTGGGAGAAGAATGGGTTTTC
                                                                                                                                                                                               ACCCCCATTACTGTGACCCTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 519)
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                                                                                                                                                                                                                                                                                                                                     h 20.7%;
Similarity 96.6%;
257; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
98 c 127 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructed by Bento Soares and M.Fatima Bonaldo."

/db_xref="GDB:1389737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares fetal liver
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="453381"
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                                                                                                                                                                                                                                                                                                                                   Score 238; DB 31;
Pred. No. 0.00e+00;
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870
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                                    408
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                                                                                                                                                                                                                                                                                                  169 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 228
                                                                                                        349
                                                                                                                                                                           289
                                                                    CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC
TTGTTATT-ATCACAA
                   TTTTTTTTATCACAA 423
                                                                                                    CAGGGTCACAGTAATGGGGGGGTTTCAAAGTGGAGA-CCACACGGCGTGCCACTGCAGTAC 407
                                                                                                                                     GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTAGCTAAATCATATAA
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                                                                                                                                                                                                         TCAGTGCATGGGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC
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2 (bases 1 to 423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-55-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiwara, T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                 h 20.6%;
Similarity 98.0%;
251; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="555E01"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="placenta"
117 c 90 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          placenta cDNA to
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                                                                                                                                                                                                                                                                                                                                               Score 236; DB 23;
Pred. No. 0.00e+00;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
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                                                                    1113
                                                                                                                                       1053
                                                                                                                                                                                                           993
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Search completed: Wed May 6 14:18:45 1998
Job time: 1066 secs.

RESULT

\*

(ME)

Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

\*

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:01:34 1998; MasPar time 9.14 Seconds 466.133 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-08-804-166-6
(1-285) from US08804166.pep
2183
1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150 Gap 11

Searched: 120837 segs, 14945562 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 31.870; Variance 121.907; scale 0.261

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2183 1 1667 1 1505 1 1306 1 1306 1 1306 1 1306 1 1306 1 1306 1 1306 1 1306 1 1307 1 1303 1 1305 1 1306 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Query Score Match Ler
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0	88
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TBP(20-190)/hCG-alpha TBP(20-161)/hCG-alpha TBP(20-190)/hCG-beta Tumour Necrosis Facto TNF-R-GBP 130 fusion TNF-alpha 55kD recept p55 TNF-R. TNF-alpha binding pro Lambda derived TNF-R. 30kD TNF inhibitor pr Human 55kD TNF-bindin TNF-R-GBP 130 fusion TNF-R-GBPH fusion pro Human Tumour Necrosis TNF-R-CBPH fusion pro TNF-R-DBPH fusion pro	Description
2.81e-227 1.50e-159 1.76e-129 2.45e-129 2.45e-129 2.45e-129 2.45e-129 2.45e-129 2.45e-129 2.45e-129 2.45e-129 2.45e-129 3.16e-129 3.16e-129 3.26e-129 3.26e-129 5.28e-129 5.28e-129 5.28e-129 5.28e-129 5.28e-129 6.81e-129 6.81e-129 7.45e-129 7.45e-129 7.45e-129 7.45e-129 7.45e-129 7.26e-129 7.26e-129 7.26e-129 7.26e-129 7.26e-129 7.26e-129 7.26e-129 7.26e-129 7.26e-129 7.26e-129 7.26e-129	Pred. No.

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61 tdcrecesgsftasenhlrhclscskcrkemggveissctvdrdtvcgcrkngyrhywse 120

Query Match Best Local S Matches 28

/ Match 100.0%; Local Similarity 100.0%; les 285; Conservative

Score 2183; DB 26; Pred. No. 2.81e-227; 0; Mismatches 0;

Length 285; Indels 0;

Gaps

0,

45	44	43	42	4.1	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
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## ALIGNMENTS

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RESULT
PR 20-FEB-1996; US-011936.

PR (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PR (ISTF) APPLIED RES SYSTEMS HOLDING NV.

PR (ISTF) APPLIED RES SYSTEMS HOLDING NV.

PR (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PR (ISTF) APPLIED RES SYSTEMS HOLDING NV.

PR (ISTE STORMS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W33359 standard; Protein; W33359; 19-MAR-1998 (first entry
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W09730161-A1.
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Fusion protein: thrombopoletin; TPO; human chorionic gonadotrophin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha subunit; hCG-alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybrid dimeric protein comprising two co-expressed units - each based on receptor or ligand and a subunit of a heterodimeric hormone, especially FSH, for inducing follicular maturation Example; Pages 32-3; 60pp; English.

A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric receptor chain or ligand, with ligand-receptor binding activity, bound directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit (hCG-alpha) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone component, reducing the requirement for hormone itself and the number of injections needed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 25
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20-FEB-1996; US-011936.
(ISTF ) ARS APPLIED RES SY
Campbell RK, Chappel SC, J
WPI; 97-455036/39.
N-PSDB; T94007.
Hybrid dimeric protein com
based on receptor or ligan
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W09730161-A1.
21-AUG-1997.
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W33357;
W33357;
19-MAR-1998
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srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd
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llarity 89.1%;
Conservative
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Pred. No. 1.50e-169;
2; Mismatches 0;
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Best Local S
Matches 19
                                                                   EP-393438-A.
24-OCT-1990; 106624.
06-APR-1990; DE-913101.
21-APR-1989; DE-920282.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT.
Hauptmann R, Himmler A, Maurer-Fo
WPI; 90-321987/43.
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W33360;
19-MAR-1998
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20-FEB-1997; U02315.
20-FEB-1996; US-011936.
(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Campbell RK, Chappel SC, Jameson BA;
WPI; 97-425036/39.
N-PSDB; T94022.
Hybrid dimeric protein comprising two co-expressed units - (
Hybrid dimeric protein comprising two co-expressed units - (
hormone, especially FSH, for inducing follicular maturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Pages 39-40; 60pp; English.

A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric receptor chain or ligand, with ligand-receptor binding activity, bound directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the thrombopoietin (PPO)/human chorionic gonadotrophin beta subunit (hCG-beta) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone component, reducing the requirement for hormone itself and the number of injections needed.

Sequence 336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA. Tumour necrosis factor binding protein; TNF-BP; TNF-recepto pTNF-BP15; infectious disease; parasitic disease; cachexia; sutoimmune disease; shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TBP(20-190)/hCG-beta fusion protein. Fusion protein; thrombopoietin; TPO; beta subunit; hCG-beta.

HOmo sapiens.
                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-1991
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DB; Q06282.
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Similarity 98.0%;
196; Conservative
TNF binding
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protein and
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d. No. 1.76e-151;
Mismatches 2;
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       HNF-
   receptor -
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PT a receptor peptide.

PS Example A: Page 53-54; 93pp; English.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite CC (Plasmodium falciparum) peptide (capable of binding to a red blood CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples CC of these hybrid peptides. R70107 is a fusion of tumour necrosis factor CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) CC and glycophorin binding protein (GBP) 130. The use of cytokine CC receptors not normally found on RBCs means that the cytokine can bind CC mannlessly to the RBC without deleterious effect. The RBC protects the CC hybrid peptides from excretion from the kidney, and due to steric CC hindrance prevents the cytokines binding to a receptor in another cell. CG BP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides cused, others include EBA 175 (175 kba erythrocyte binding antigen), CC receptor molecule (eg. exhibited by plasmodium vivax). These peptides CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on CC the surface of fRBCs. The hybrid peptides are thus used to lower C the levels of free cytokines in the circulation to reduce pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 16
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09-MAR-1995.

01-SEP-1994; G01900.

03-SEP-1993; GB-018350.

23-AUG-1994; GB-017021.

(PREN/) PRENDERGAST K F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R70107 stand
R70107;
R70107;
10-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour treatment and to understand mechanismsm to TNF action Disclosure; Fig 1(1-3); Slpp; German.
Clone pTNF-BPI5 was used to contruct paDTNF-BP, for transfection of e.g. COS7 cells. The expressed proteins are useful prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or beta (e.g. infectious or parasitic diseases, shock, cachexia, autoimmune diseases, adult respiratory distress syndrome etc., or side effects of treatment with TNG-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions. See also Q06382-Q06285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF-R-GBP 130 fusion protein.

TNF-R-GBP 130 fusion protein.

Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cycokine receptor; glycophorin binding peptide 130; cnp 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GBP 130; GBPH; glycop
Chimeric Homo sapiens
Chimeric Plasmodium f
                                                                                                                                                                                                                                                                                                                                                                                                                     New hybrid peptide(s) for binding cytokine(s) - malaria parasite peptide capable of binding a re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prendergast KF;
WPI; 95-115452/15.
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1 Similarity 98.8%;
169; Conservative
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Pred. No. 2.45e-129;
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a red blood cel
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Query Match

59

Score

1305;

B 13;

Length 451

l Similarity 169; Conser

Length 455 Indels

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                                                    PT New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.

PS Example; Fig 1: 43pp; English.

CC 7111 Sequence was deduced from human TNF-alpha cDNA isolated as in C24440. The first 35 amino acids are generally quite hydrophobic and probably represent a signal sequence. Residues 35-40 are highly charged (DREKR) and this is not normally found in secretory signal sequences. It is possible the receptor is processed by proteolysis after residue 40 which contains a dibasic cleavage site (KR). Hydropathy analysis of this sequence predicts a single transmembrane domain of 23 amino acids, dividing the sequence into an extracellular domain of 171 residues and a cytoplasmic domain of 221 residues. The sequence contains a large number of cysteine residues, the arrangement of which is similar to that of other cell surface proteins, suggesting the TNF-alpha receptor is structurally related to a family of receptors.

NOTE: - Residues 371,2 given in the sequence as T,L, are encoded by Sequence 455 AA;
Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.3%; Matches 169; Conservative
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18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS SU
Brennan FM, Feldmann M,
WPI; 92-167156/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis factor alpha; extracellular binding domain; treatment; pulmonary diseases; septic shock; HIV infection; malaria; viral meningits; graft versus host disease; autoimmune disease; rheumatoid arthritis.
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R24000;
05-NOV-1992 (fir
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18-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "potential"
212..234
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145..147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= signal peptide 54..56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= N linked glycosylation site
/note= "potential"
151. 153
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             59.8%;
98.8%;
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M, Gray PW,
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Score 1306; DB 4;
Pred. No. 2.45e-129;
1; Mismatches 1;
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Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                          MJC;
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PT antagonising deleverious carriers.

S Disclosure; Fig 1; 40pp; English.

C This sequence represents human p55 tumour necrosis factor (TNF-R).

C Expression of this receptor is regulated by shedding of the extracellular conditions of the receptor fragment. The p55 TNF-R can be shed in response to different conducting agents, e.g. phorbol myristate accetate (PMA), depending on cell conducting agents, e.g. phorbol myristate accetate (PMA), depending on cell conducting agents, e.g. phorbol myristate accetate (PMA), depending on cell conducting agents, e.g. phorbol myristate accetate (PMA), depending on cell conducting agents, e.g. phorbol myristate accetate (PMA), depending on cell conducting agents, e.g. phorbol myristate accetate (PMA), depending on cell conducting agents, e.g. phorbol myristate accetate (PMA), depending on cell conducting response is the spacer region (see R75012) in the extracellular conduction and links the Cys rich module to the transmembrane domain. The spacer region of the transmembrane domain. The conduction of the exceptor and substitutions consultations (R5013-25) and substitutions consultations (R75013-25) and substitutions consultations (R75013-25) and substitutions are consultations (R75013-25) and substitutions consultations (R75013-25) and substitutions are consultations (R75013-25) and substitutions (R
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                                                                                                                                                                                                                                                                                                                                                                                  New protease capable of cleaving soluble tumour necrosis factor (TNF) receptor - from cell-bound TNF- receptor, useful for antagonising deleterious effects of TNF.
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Batkin M, Brakebusch C, Varfolomeev E,
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R75084;
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N-PSDB; Q90513.
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  identity of these residues, on the identity of Val 173.
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201
/note= "major C termin
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193..210
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198..210
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54..56
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  Mutations
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Best Local S
Matches 16
               Query Match
Best Local :
  Matches
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15-JUN-1990; 013410.
15-JUN-1990; GB-013410.
(CHAR-) CHARING CROSS SUNLE.
Feldman M, Gray P, Turner M, E
WPI; 92-043613/06.
                                                                             e.g. rheumatoid arthritis
Disclosure; Fig 1; 25pp; English.
The amino acid sequence is that of tumour necrosis factor alpha
binding protein which contains the extracellular domain of human T
alpha receptor. It is soluble and can be used in the regulation of
TNF-mediated responses by binding and sequestering the cytokine. I
can therefore be used therapeutically to treat disorders such as
cachaxia, sepsis and autoimmune diseases, specifically rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conformation of the protein adversely effect the shedding process. The mutations shown in R75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNF-R from the cell bound TNF-R. Fragments of these inhibitors can be seen in R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can be used for enhancing TNF function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis extracellular do
                                                        Sequence
                                                                    arthritis.
                                                                                                                                                                                          New tumour necrosis factor alpha binding protein and polypeptide useful in treating cachexia, sepsis and auto immune diseases
                                                                                                                                                                                                                      N-PSDB; Q20973
                                                                                                                                                                                                                                                                                                                                                                  modified_site
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R20787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
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               Similarity
                                                      455 AA;
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  Conservative
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212..234
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factor alpha; autoimmune
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                                                                                                                                                                                                                                                                                                                                                     'note- "potential N-glycosylation site"
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1; M
Score 1306; DB 4; )
Pred. No. 2.45e-129;
1; Mismatches 1;
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No. 2.45e-129;
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                            Length 455;
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Matches 16
                                                                                                                                                                                     The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses
                                                                                                                                                                                                                                                                                                                                                                                New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Disclosure; Page 57-59; 85pp; English.

The sequences given in R42058-59 repressent human tumour necrosis factor receptor (TINF-R) and the sequences in R42060-61 represent human interleukin-1 receptor (IL-IR). These sequences were used the production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) II
Smith CA;
                                                                                                                                                              autoimmune
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                                                                                                                                                                                                                                                                                                                             IL-1R-linker-TNF-R-linker-TNF-R
TNF-R-linker-TNF-R
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26-MAR-1993; U02938.
30-MAR-1992; US-860710.
(IMMV ) IMMUNEX CORP.
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                                                                                                                                                                           disease, sepsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KONTYCTCHAGFFLRENECYSCSNCKKSLECTKLSLPQIENYKGTEDSGTT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYMSENLFQCFNCTLCLNGTVHLSCQE
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41..455
/note= "Mature hTNF-R"
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98.8%;
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Best Local
                                                                                                                                                                                                                                                              Human 55kD TNF-binding protein.
Tumour Necrosis Factor; binding
autoimmune glomerulonephritis; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour necrosis factor inhibitor - for suppression of TNF-alpl
and -beta, useful as therapeutic agent.
Disclosure; Fig 21; 142pp; English.
The sequence comprises the entire 30 kD TNF inhibitor. The cla
from which the sequence was deduced was isolated from a cDNA
library prepd. from RNA form U937 cells treated with PMA/PHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The whole gene can be inserted into expression vectors for prepnof TNF inhibitor for use in the treatment of inflammatory and degenerative diseases. The active protein is claimed (Claim 8). See also R10984 and R11001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1990; 058976.
18-JUL-1989; US-381080.
11-DEC-1989; US-450329.
07-FEB-1990; US-479661.
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Pred. No. 2.45e-129;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                 j proteins; septic shock;
lymphokine; cytokine.
                         N-glycosylation
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Matches 16
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Claim 1; Fig 1; 26pp; German.
Partial amino acid sequences were determined for the 55 and 75kD
TNF-BPs (see R11072-R11081) and oligonucleotide primers were
synthesised based on these partial sequences. The primers were used
to produce a cDNA fragment for use as aprobe to screen a human
placental cDNA bank constructed in lambda gtll. Positive clones were
identified and sequenced. DNA constructs comprising the TNF-BP coding
sequence may also contain a fragment encoding a human ig domain.
Recombinant constructs are used to transform cells to confer
improved TNF-binding properties.
                                                                                                                                                                                                                                                  W09506737-A.
09-MAR-1995
01-SEP-1994; G01900.
03-SEP-1993; GB-018350.
23-AUG-1994; GB-017021.
(PREN/) PRENDERGAST K F.
New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell and a receptor peptide.

Example A; Page 46-47; 93pp; English.

Example A; Page 46-47; 93pp; English.

Example Air page 45-47; 93pp; English.

Example Air page 45-4
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N-PSDB; Q10955.
Insoluble tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                           TNF-R-CBP 130 fusion protein.
TNF-R-CBP 130 fusion protein;
Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
red blood cell; cytokine receptor; glycophorin binding peptide 130;
red blood cell; cytokine receptor; plycophorin binding peptide homologue; glycophorin A.
                                                                                                                                                                                                          Prendergast KF;
WPI; 95-115452/15.
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Schlaeger EJ;
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12-SEP-1989; CH-003319.
08-MAR-1990; CH-000746.
20-APR-1990; CH-001347.
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20-MAR-1991.
                                                                                                                                                                                                                                                                                                                                                                                           Chimeric Plasmodium
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Llarity 98.8%;
Conservative
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/label= signal peptide
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Pred. No. 2.45e-129;
1; Mismatches 1;
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prods. and :
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PT a receptor peptide.

PS Example A; Page 54-55; 93pp; English.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite CC (Plasmodium falciparum) peptide (capable of binding to a red blood CC (Plasmodium falciparum) peptide are claimed. R70103-25 are examples CC (Plasmodium falciparum) peptide are claimed. R70103-25 are examples CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples CC of these hybrid peptides. R70108 is a fusion of tumour necrosis factor CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) CC and glycophorin binding protein (GBP) homologue (GBPH). The CC use of cytokine receptors not normally found on RBCs means that the CC cytokine can bind harmlessly to the RBC without deleterious effect. CC The RBC protects the hybrid peptides from excretion from the kidney, and CC due to steric hindrance prevents the cytokines binding to a receptor in CC another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides cused, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA 'New Amalaria parasite peptides cused, others include EBA 175 (175 kDa erythrocyte binding raceptor in the cytokines binding antigen), PMMSA 'New Amalaria parasite peptides cused, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA 'New Amalaria parasite peptides cused, others include surface antigen) and the Duffy binding raceptor
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Best Local S
Matches 16
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01-SEP-1993; GB-018350.
03-SEP-1993; GB-017021.
23-AUG-1994; GB-017021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF-R-GBPH fusion protein.

Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cytokine receptor; glycophorin binding peptide 130; GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A; tumour necrosis factor receptor; TNF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               harmlessly to the RBC without deleterious effect. The RBC protects the hybrid peptides from excretion from the kidney, and due to steric hindrance prevents the cytckines binding to a receptor in another cell. GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptide used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major merozoite surface antigen) and the Duffy binding receptor molecule (eg. exhibited by Plasmodium vivax). These peptides bind to pref. glycophorin A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid peptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R70108
R70108;
                                                                                                                                                                                                                                                                                                                       New hybrid peptide(s) for binding malaria parasite peptide capable c
                                                                                                                                                                                                                                                                                                                                                                 Prendergast KF;
WPI; 95-115452/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key Location/Qualifiers misc_difference 230..269
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Chimeric Plasmodium falciparum.
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on RBCs means
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3.16e-129;
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                                                                                                                                                                                                                DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanismsm to TNF action Disclosure; Fig 91(1-2); 51pp; German.

C IAMDGATNF-R8 (Q06584) was used to screen the HS913T cDNA library.

C LAMDGATNF-R2 encodes the complete human TNF-R2 and was used to construct a plasmid (pADTNF-R) expressing the product the same way as pADTNF-BP (see Q065282). The expressed proteins are useful prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock, cachexia, autoimmune diseases, adult respiratory distress syndrome etc., or side effects of treatment with TNG-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions.

See also Q06282-Q06285.
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert. Tumour necrosis factor binding protein; TNF-BP; TNF-receptor; Infectious disease; parasitic disease; cachexia; autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT
                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q06285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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llarity 98.2%;
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98.28;
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                                                                                                                                                             Score 1303; DB 2;
Pred. No. 5.28e-129;
2; Mismatches 1;
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Pred. No. 5.28e-129;
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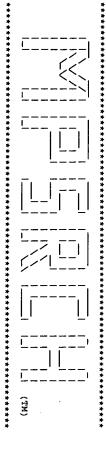
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PI Prendergast KF;
PI Prendergast KF;
PI Prendergast KF;
PI New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell and PT malaria parasite peptide capable of binding a malaria parasite (c) PT malaria parasite peptides for binding cytokines, comprising a malaria parasite (C) Plasmodium falciparum) peptide (capable of binding to a red blood (c) cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples (C) of these hybrid peptides. R70104 is a fusion of tumour necrosis factor receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) (c) and glycophorin binding protein (GBP) homologue (GBPH). The use of CC cytokine receptors not normally found on RBCs means that the CC cytokine receptors the hybrid peptides from excretion from the kidney, and CC used others include EBA 175 (175 kDa erythrocyte binding antigen), pMMSA (pre major merozoite surface antigen) and the Duffy binding receptor consecute (eg. exhibited by Plasmodium vivax). These peptides bind to C pref. glycophorin A, B and C, sialo glycoproteins, found on the surface cytokines in the circulation to reduce pathological damage.

Sequence 547 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 16
                  143
                                                                                                                                   83
                                                                                                                                                                                               90
                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                      20
                                                                                                                             scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
                                               kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts 190
                                                                                                                                                                                                                                                           dsvcpqgkyihpqnnsicctkchkgtylyndcpgppgqdtdcrecesgsftasenhlrhcl
KONTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT
                                                                                                                                                                                                                                                                                                                                                                               ch 59.7%;
l Similarity 98.2%;
168; Conservative
                                                                                                                                                                                                                                                                                                                                                                               Score 1303; DB 13;
Pred. No. 5.28e-129;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                   79
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Wed May 6 09:00:43 1998; MasPar time 12.89 Seconds 807.727 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-804-166-6 (1-285) from US08804166.pep 2183

1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150 Gap 11

Searched:

120446 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 40.957; Variance 71.278; scale 0.575

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

		ø					
No.	Score	Query Match	Length	BB	Ħ		z
ь ¦	1306		455	<u> </u>	GQHUT1	tumor necrosis factor	1.60e-278
N	1241	56.8	160	ر.	1EXTA	necrosis	σ
ω	1222	•	158	ഗ	1EXTB	tumor necrosis factor	
4	1119	•	142	s	INCFB		. 286
ហ	1103	٠	139	S	1TNRR		. 62e
σ	1096		140	s	1NCFA	tumor necrosis factor	
7	1012		461	N	JC4302	tumor necrosis factor	1.20e-207
00	944	٠	454	N	I57826	tumor necrosis factor	2.33e-191
ی ا	944	•	454	-	GQMST1	tumor necrosis factor	2.33e-191
10	928	•	461	۳	GQRTT1	tumor necrosis factor	1.56e-187
:::	672	•	116	۳	TTHUAP	glycoprotein hormones	
12	650	•	86	U	1HRPA	chorionic gonadotropi	1.23e-121
13	648	٠	85	G	LXULA	chorionic gonadotropi	
14	648	•	85	u	1 HCNA	Human chorionic gonad	3.63e-121
15	552	25.3	120	N	A39555	glycoprotein hormones	8.95e-99
16	547	25.1	96	N	A05096	glycoprotein hormones	. 29e
17	549	•	120	_	TTBOA	glycoprotein hormones	4.44e-98
18	549	25.1	120	μ	UTSHA		4.44e-98
19	544	٠	120	Н	TTRTA	glycoprotein hormones	6.39e-97
20	542	•	96	N	PN0138	glycoprotein hormones	-9
21	542	٠	120	_	UTPGA	glycoprotein hormones	. 86e
22	542	•	120	_	TTMSA	glycoprotein hormones	9
23	540	24.7	120	N	G00021	chorionic gonadotropi	.39e-9

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
212	214	221	225	228	245	434	448	448	450	452	474	479	478	500	500	500	503	505	507	537	53/
9.7	9.8	10.1	10.3	10.4	11.2	•	20.5	•	20.6	20.7	21.7	21.9	•	22.9	22.9				23.2	•	•
427	349	326	325	38	435	117	114	108	114	119	117	97	93	118	118	118	96	120	118	120	D2.T
۲	N	μ.	N	N	N	N	N	N	N	ຎ	N	N	N	N	_	N	_	N	Ŋ	N	٨
GQHUN	D36858	GQVZML	B43692	A60583	I54182	150992	I51230	A60627	в60627	151229	A37198	S20287	S07091	A60626	UTCAA	S16762	TTHOA	S53062	A40554	I51241	A45585
nerve growth factor r	gene G4R protein – va	T2 protein - myxoma v	T2 protein - rabbit f	glycoprotein hormones	tumor necrosis factor	-	gonadotropin alpha 2	glycoprotein hormones	glycoprotein hormones	gonadotropin alpha l	glycoprotein hormones	ha chain	glycoprotein hormones	glycoprotein hormones	glycoprotein hormones	gonadotropin alpha ch	glycoprotein hormones	glycoprotein hormones	glycoprotein hormones	pituitary glycoprotei	glycoprotein normones
3.08e-23	1.20e-23	4.42e-25	6.62e-26	1.59e-26	4.53e-30	1.13e-71	7.40e-75	7.40e-75	2.59e-75	9.07e-76	8.53e-81	6.10e-82	1.03e-81	9.19e-87		9.19e-87	1.88e-87	6.50e-88	2.25e-88	2.67e-95	2.6/e-95

# ALIGNMENTS

RESULT

##cross-references GB:M33294; NID:g339744; PID:g339745	## CI
esidues 1-455 ##label SCH	##10
##molecule_type mRNA	##mc
sion A34900	#accession
#cross-references MUID:90235285	#cross-
factor.	
	#title
	#journal
H.; Kohr, W.J.; Goeddel, D.V.	:
Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,	
Schall, T.J.; Lewis, M.; Koller, K.J.;	#authors
A34900	REFERENCE
mature protein, confirmed by protein sequencing	
ote part of this sequence, including the amino end of the	##nc
##experimental_source placenta	##ey
##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754	##CI
##residues 1-455 ##label LOE	97##
##molecule_type mRNA	# #mc
Sion A34899	#accession
references MUID:90235284	#cross-
necrosis factor receptor.	
Molecular cloning and expression of the human 55 kd tumor	#title
Cell (1990) 61:351-359	#journal
	:
ť	#authors
A34899	REFERENCE
##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;	##CI
FUC	##re
_type DNA	##mc
sion A38208	#accession
	#title
Genomics (1992) 13:219-224	#journal
	#authors
	REFERENCE
38280; A34899; A34900; A36333; A36281; S12037; JT0758; A60231; A38258; A60594; A35010; JC2404	ACCESSIONS
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change	DATE
#formal_name Homo sapiens #common_name man	ORGANISM
binding protein 1 (TNF blocking factor)	
tumor necrosis factor receptor type 1 precursor - humanALTERNATE_NAM tumor necrosis factor alpha inhibitor: tumor necrosis factor	TITLE
GQHUT1 #type complete	ENTRY

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REFERENCE
                                                                                                                                                                                                                                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors #journal
                                                                                                                                                                                                                                                #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwar R.; Aderka, D.; Holtmann, H.; Wallach, D.
#journal EMBO J. (1990) 9:3269-3278

*title Soluble forms of tumor necrosis factor receptors (TNF-Rs).
The CDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.

*cross-references MUID:91006021

*accession S12057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#title Cloning of human tumor necrosis factor (TNF) receptor CDNA
and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A38281
                                                                                                                                                    #cross-references MUID:90292116
#accession A60231
                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                                                      #accession
                                                                                                                                                                                                                                                                                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type protein
##residues 30-38;41-53,'x',55-79,'xx',82-94,'NK';'xx',100-104;
##residues 107-128;162-167,'X',169-201 ##label HI2

the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##IIOLIECTIVE ........
##ICTOSS-references EMBL:X55313; NID:g37223; PID:g37224
##rote parts of soluble TNF binding protein 1,
##note amino and carboxyl ends, were confirm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-455 ##label
##cross-references GB:M63121;
cession C36555
##molecular
                                                                                                   **residues
                                                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                    ##molecule_type protein
                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1-455 ##label GRA
##cross-references GB:M37764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
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Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
R.S.; Granger, G.A.
                                                                                                                                                                                         Eur. J. Immunol. (1990) 20:1167-1174
Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.
                                                                                                                                                                                                                                                                                                                                                                                                                 JT0758

Kemper, O.; Wallach, D.
Gene (1993) 134:209-216

Cloning and partial characterization of the promoter human p55 tumor necrosis factor (TNF) receptor.

JT0758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A38281
Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
                                                                            A38258
                                                                                                                                                                                                                                                                                                                   Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield,
                                                                                                                                                                                                                                                                                                                                              A60231
                                                                                                                                                                                                                                                                                            Ċ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Leu, and GAC for residue 427 as Asn
                                                                                                   41-43,'X',45-53,'X',55-57 ##label SEC
                                                                                                                                                                                                                                                                                                                                                                  1-13 ##label KEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIM
NID:g339755; PID:g339756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding protein 1, including its ends, were confirmed by protein
                                                                                                                                                                                                                                                                                                           P.; Dayer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H.; Zwang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
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FEATURE
1-21
                                                                                                             SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENETICS
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                           Query Match
Best Local
     Matches
                                                                                                                                                                                                               84-126
127-167
168-196
212-234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references GDB:125913; OMIM:191190

#map_position 12p13.2-12p13.2

#introns 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1

#SUPERFAMILY tumor necrosis factor receptor type 1; NGF

receptor repeat homology

receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #journal
#title
                                                                                                                                                                                                                                                                                                                                                                         30-211
41-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors
                                                                                                                                                              54,145,151
                                                                                                                                                                                                                                                                                                                       44-82
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#urification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.

#cross-references MUID:91062364

#accession A38258
                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-455
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#accession A35010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##experimental_source urine
This protein is one of two known receptors
(cachectin) and TNF-beta (lymphotoxin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##experimental_source normal urine
PNCE JC2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type protein
##residues 41-43,'X',45-53,'V',55-57,'XK',60
##experimental_source renal failure patient urine
ENCE A35010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##experimental_source cancer patient serum NCE A60594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type protein
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##residues 41-45 ##label ENG
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                           y Match 59.8%; Local Similarity 98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type protein
##residues 41-53,'x',55-144,'x',146-150,'x',152-186,'x',188-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, Grubb, A.; Adolf, G.
Eur. J. Haematol. (1989) 42:270-275
Isolation and characterization of a tumor ne binding protein from urine.
A60594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kejihara, J.; Asada, A.; Kirihara, S.; Kato, K. Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. (1990) 265:1531-1536
Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JC2404
                                                                                                       #length 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  duplication; glycoprotein; receptor; transmembrane protein
  Conservative
                                                                                                                                                   #domain extracellular *status predicted *label EXT\
*product TWF binding protein 1 (tumor necrosis factor
alpha inhibitor) *status experimental *label TBP1\
*domain NGF receptor repeat homology *label NG2\
*domain NGF receptor repeat homology *label NG3\
*domain NGF receptor repeat homology *label NG3\
*domain NGF receptor repeat homology *label NG4\
*domain NGF receptor repeat homology *label NG4\
*domain NGF receptor repeat homology *label NG4\
*domain intracellular *status predicted *label NEM\
*domain intracellular *status predicted *label INT\
*binding_site carbohydrate (Asn) (covalent) *status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41-60 ##label GAT
                                                                                                                                                                                                                                                                                                                                                                                                                          #domain signal sequence #status predicted #label SIG\
#product tumor necrosis factor receptor type 1 #statu
predicted #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##label KAJ
                                                                                                                                   predicted
                                                                                                       #molecular-weight 50494 #checksum 153
                        Score 1306; DB 1; Pred. No. 1.60e-278;
  1; Mismatches
                                                 Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for both TNF-alpha
  Indels 0;
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Determination: X-ray diffrac
R-value: no refinement
binding protein: core---
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Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for
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Crystallographic evidence for dimerization of unliganded tumor necrosis factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor receptor extracellular domain, chain a extracellular domain of the 55kda tumor necrosis factor receptor. crystallized at ph3.7 in p 21 21 and a sepressed in Escherichia coli, the construct contains residues 12 to 172 of the mature sequence of the entire receptor. residue 11 is mutated to met as a result of the

    K.: Naismith, J.H.; Sprang, S.R.
    J. Mol. Biol. (1994) 239:332
    Two crystal forms of the extracellular domain of type i tumor necrosis factor receptor.

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#authors
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133-136,139-142
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binding protein; cytokine;
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Resolution: 1.85 angeton
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158; Conservative
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Cell (1993) 73:431-445
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J. Mol. Biol. (1994) 239:332

Two crystal forms of the extracellular domain of necrosis factor receptor.
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                1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
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VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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Determination: X-ray diffraction
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Similarity 99.3%;
141; Conservative
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  binding protein;
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Similarity 98.7%;
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Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for
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J. Mol. Biol. (1994) 239:332
Two crystal forms of the extracellular domain
necrosis factor receptor.
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#disulfide_bonds 
#length 158 #molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.;
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
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contains residues 12 172 of the mature receptor sequence
chain B - hu
                                                                                                                                 #length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                             Score 1119; DB 5; Pred. No. 2.28e-233; 1; Mismatches 0;
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Pred. No. 3.27e-258;
1; Mismatches 1;
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KEYWORDS
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D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.
Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.;
Lesslauer, W.

J. Mol. Biol. (1993) 229:555

Crystallization and preliminary analysis of tnf
tnf-beta-55 kd tnf receptor complex.

Resolution: 2.85 angstroms
Determination: X-ray diffraction
                                                                                                                                                                                                                                                                                                     h 50.5%;
Similarity 99.3%;
138; Conservative
tumor necrosis factor receptor 55 kd extracellular domain
contains residues 12 172 of the mature receptor sequence,
chain A - hu
stnfr1; type i receptor
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H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
Cell (1993) 73:431-445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banner, D.W. submitted to
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                                                                                                                                                                                                                                                                                                     Score 1103; DB 5;
Pred. No. 1.62e-229;
1; Mismatches 0;
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               1-461 ##label
##cross-references GB:U19994;
:cession PC4093
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   ##residues
           ##molecule_type
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                                                         ##molecule_type mRNA
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Local Similarity 99.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor activation.
Resolution: 2.25 angstroms
Determination: X-ray diffraction
R-value: no refinement
binding protein; cytokine;
                                                                                        Suter, B.; Pauli, U.
Gene (1995) 163:263-266
Cloning of the CDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A40737
Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.;
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
Cell (1993) 73:431-445
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Two crystal forms of the extracellular domain of necrosis factor receptor.
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expressed in Escherichia coli, residue 11 is
                                                                        JC4302
                                                                                                                                                                 tumor necrosis factor receptor p55 - pigoRGANISM 29-Nov-1995 #sequence_revision 08-Feb-1996 #text
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Pred. No. 7.85e-228;
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NID:g1141752;
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                                   PID:g1141753
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##cross-references GB:M76656;
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101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
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Local Similarity 71.9%;
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                                                                                                                                                                                                                            ch 43.2%;
l similarity 67.4%;
ll6; Conservative
                                                                                                                                                                                                                                                                                                                                                                        13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1 superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology cytokine receptor cytokine receptor superfamily functional superfamily cytokine receptor superfamily super
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Genomic organization and promoter function of
tumor necrossis factor receptor beta gene.
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glycoprotein; kidney; receptor; transmembrane protein; tumor
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Steinmetz, M.
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Pred. No. 2.33e-19
28; Mismatches 2
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NID:g202100; PID:g202102
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#title Molecular cloning and expression of the type 1 and type murine receptors for tumor necrosis factor.
#cross-references MUID:91246168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.
#cross-references MUID:91187885
                                                                                                                           #journal Immunogenetics (1994) 39:450-451
#title Nucleotide sequence of the TNF t:
endothelioma cell line.
#cross-references MUID:94245292
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#residues 1-454 ##label ROT
##cross-references EMBL:X57796; N
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##cross-references GB:M60468; NID:g199825; PID:g199826
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##residues 1 - 454 ##label RES
##cross-references GB:L26349; NID:g430732; PID:g430733
This protein is one of two distantly related receptors
TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES #formal_name Mus musculus #common_name house mouse 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                  S19021
                                                                                                                                                                                                                                                                                                                                                                       Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, Immunogenetics (1991) 34:338-340
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Query Match 43.2%;
Best Local Similarity 67.4%;
Matches 116; Conservative
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Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
Stratowa, C.; Adolf, G.R.
#journal DNA Cell Biol. (1990) 9:705-715
Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
#accession B36555
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##cross-references GB:M6312; NID:g207361; PID:g207362
This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxin).

IFICATION #superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology
duplication; glycoprotein; receptor; transmembrane protein
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J. Mol. Appl. Genet. (1981) 1:3-18

#title The gene encoding the common alpha

glycoprotein hormones.

#cross-references_MUID:82267643
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##residues 1-116 ##label FID
##cross-references GB:V00518; NID:g31868; PID:g31869
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Sairam,
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Fiddes, J.C.; Goodman, H.M
Nature (1979) 281:351-356
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alpha chain; follitropin alpha chain; interstitial
cell-stimulating hormone alpha chain; luteinizing hormone
alpha chain; lutropin alpha chain; thyroid-stimulating
hormone alpha chain; thyrotropin alpha chain
formal_name Homo sapiens #common_name man
13-Jul-1981 #sequence_revision 23-Oct-1981 #text_change
                                                                                                                                                                                                                                                                             Birken, S.; Fetherston, J.; Canfield, R.; Boime, I. J. Blol. Chem. (1981) 256:1816-1823
The amino acid sequences of the prepeptides contained in alpha and beta subunits of human choriogonadotropin.
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                                          restriction endonuclease evidence indicates that a single gene codes for the alpha chain common to the four dimeric hormones: thyrotropin, lutropin, follitropin, and choriogonadotropin previously the mature alpha chain (residues 25-116) was isolated from each of the hormones and its sequence was determined, as documented below
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Fauthors Shome, B.; Parlow, A.F.
#Journal J. Clin. Endocrinol. Metab. (1974) 39:199-202
#title Human follicle stimulating hormone (hrsH): first proposal
the amino acid sequence of the alpha-subunit (hrsHalpha)
and first demonstration of its identity with the
alpha-subunit of human luteinizing hormone (hLHalpha).
#cross-references MUID:74262937
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#journal J. Biol. Chem. (1975) 250:5247-5258
#title The amino acid sequence of human chorion
alpha subunit and beta subunit.
#cross-references MUID:75211304
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#title
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#journal J. Biol. Chem. (1975) 250:6735-6746
#title Primary amino acid sequence of follicle-stimulating hormone
#title from human pituitary glands.
#cross-references MUID:76005558
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#journal Biochem. Biophys. Res. Commun. (1972) 48:530-537
#title Human pituitary interstitial cell stimulating hormone:
    primary structure of the alpha subunit.
#cross-references_MUID:72242988
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#accession A90751
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##residues 25-116 ##label BEL
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##residues 28-107,'SC',110-116 ##label SA2
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##residues 28-107,'SC',110-116 ##label SAI
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##residues 25-116 ##label MOR
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Structure of human luteninizing hormone.
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                   Fujiki, Y.; Rathnam, P.; Saxena, B.B. Biochim. Biophys. Acta (1980) 624:428-43 Studies on the disulfide bonds in human
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Approximately 1-2 and 1-3,

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*authors Lapthorn, A.
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#contents annotation; prelinerance A44674
    COMMENT
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56-108,83-111
76,102
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##cross-references GDB:119774; OMIM:118850
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##molecule_type DNA

##residues 1-116 ##label RES

##cross-references GB:S70585; NID:g546844; PID:g546845
                                                                                                                                                                                                                                                                                                                                                                      253 CVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS
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Similarity 93.5%;
87; Conservative
                                                                                         Nature (1994) 369:455
Crystal structure of human chorionic gonadotropin.
TN022063
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                          J. Biol. Chem. (1989) 264:6705 Preliminary x-ray diffraction analysis of human chorionic
                                                                                                                                                  Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; J.W.; Canfield, R.E.; Machin, K.J.; Morgan,
                                                                                                                                                                                                               Lapthorn, A.J.; Harris, D.C. submitted to the Brookhaven
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Nippon Rinsho (1994) 52:940-947
[Structure and regulation of human thyroid-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature (1994) 369:455-461
Crystal structure of human chorionic gonadotropin.
annotation; X-ray crystallography, 3.0 angstroms;
of disulfide bonds
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Protein Data Bank, August 1994
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F.J.; Isaacs,
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CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLYQKNVTSESTCCVAKSYN 259
                                               CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
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Determination: theoretical model
complex; glycoprotein hormone
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Similarity 96.5%;
83; Conservative
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Similarity 100.0%;
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Structure (London) (1996) 3:1341
Structural predictions for the ligand-binding region glycoprotein hormone receptors and the nature of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N. submitted to the Brookhaven Protein Data Bank, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield,
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Pred. No. 3.63e-121;
0; Mismatches 0;
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                                                                                                                                           #authors Golos, T.G.; Durning, M.; Fisher, J.M.
#journal DNA Cell Biol. (1991) 10:367-380
#title Molecular cloning of the rhesus glycoprotein hormone
#cross-references MUID:91321740
#accession A39555
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3-27
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                                                                                                    ##molecule_type DNA ##residues 1-120 ##1aba1 ^^*
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Local Similarity 100.0%; Pred. No. 3.63e-121;
les 83; Conservative 0; Mismatches 0;
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Resolution: 2.6 angstroms
Determination: X-ray diffraction
                                                        1-120 ##label GOL

#superfamily glycoprotein hormones alpha chain

glycoprotein

#length 120 #molecular-weight 13785 #checksum
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Structure (1994) 2:545

Structure of human chorionic gonadotropin at 2.6 angstroms resolution from mad analysis of the selenomethionyl
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 25.3%;
llarity 83.5%;
Conservative
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Score 552; DB 2; Length 120;
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4; Mismatches 10; Indels
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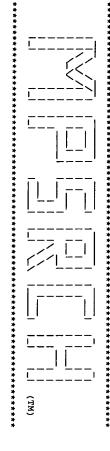
35 CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT 94

Search completed: Wed May 6 09:01:17 1998 Job time: 34 secs.

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260 RYTYMGGFKVENHTACHCSTCYYHK 284

(OT92U) AMAJO SUAS SIHT



Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Run on: Wed May 6 08:58:14 1998; MasPar time 8.40 Seconds 851.426 Million cell updates/sec

Tabular output not generated.
Title: >US-08-804-166-6

Title: >US-08-804-166-6

Description: (1-285) from US08804166.pep

Perfect Score: 2183

Sequence: 1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
Gap 11

Searched: 69112 seqs, 25083644 residues
Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 42.622; Variance 62.749; scale 0.679

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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GLYCOPROTEIN HORMONES	. –	GLYCOPROTEIN HORMONES		GLYCOPROTEIN HORMONES	TUMOR NECROSIS FACTOR	TUMOR NECROSIS FACTOR	TUMOR NECROSIS FACTOR	TUMOR NECROSIS FACTOR	Description													
5.13e-102			6.51e-104	.57e-	8.55e-112	6.95e-113	1.30e-112	1.98e-113	1.98e-113			. 646	2.44e-115			3.70e-116		8.75e-221	2.69e-225	1.63e-244	0.00e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	28	27	26	25	24
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8.4	8.7	9.3	9.7	9.7	9.7	9.8	9.9	10.1	10.3	11.2	11.3	17.2	19.4	19.6	20.5	20.6	21.7	21.9	21.9	22.9	22.9
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CD30_HUMAN	FASA_BOVIN	CD27_HUMAN	TNR2_MOUSE	NGFR_HUMAN	NGFR_RAT	VC22_VARV	TNRC_MOUSE	VT2_MYXVL	VT2_SFVKA	TNRC_HUMAN	WSL1_HUMAN	GLHA_FUNHE	GLHA_ACALA	GLHA_THUOB	GLH1_ONCKE	GLH2_ONCKE	GLHA_ANGAN	GLHA_RANCA	GLHA_MURCI	GLHA_CTEID	GLH1_CYPCA
CD30L RECEPTOR PRECURS	FASL RECEPTOR PRECURSO	CD27L RECEPTOR PRECURS	TUMOR NECROSIS FACTOR	LOW-AFFINITY NERVE GRO	LOW-AFFINITY NERVE GRO	PROTEIN C22/B28 HOMOLO	LYMPHOTOXIN-BETA RECEP	TUMOR NECROSIS FACTOR	TUMOR NECROSIS FACTOR	LYMPHOTOXIN-BETA RECEP	WSL-1 PROTEIN PRECURSO	GLYCOPROTEIN HORMONES									
1.24e-20	1.77e-22	1.61e-25		2.04e-27		6.80e-28	2.26e-28		1.55e-30	2.07e-35	6.68e-36	6.97e-69	1.37e-81	2.17e-82	.27e-	1.53e-88	5.42e-95	2.43e-96	4.53e-96	5.13e-102	5.13e-102

# ALIGNMENTS

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CC -!- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGER/TNER-TYPE CYSTEINE-RICH REGION.

CC -!- SIMILARITY CONTAINS A LA-NGER/TNER-TYPE CYSTEINE-RICH REGION.

CC -!
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AN ARISMITH J.H., DEVINE T.O., KHONO H., SPRANG S.R.;

AN ARISMITH J.H., DEVINE T.O., KHONO H., SPRANG S.R.;

AN ARISMITH J.H., DEVINE T.O., KHONO H., SPRANG S.R.;

AN ARISMITH J.H., DEVINE T.O., KHONO H., SPRANG S.R.;

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AN ARISMITH J.H., DEVINE T.O., KHONO H., SPRANTOR MOLECULE FADD

C. I. FUNCTION: RECEPTOR FOR THE DEATH INDUCING SIGNALING COMPLEX (DISC)

C. PERFORMS CASPAGE-8 PROTEDLYTIC ACTIVATION WHICH INTITIES THE

C. PERFORMS CASPAGE-8 PROTEDLYTIC ACTIVATION WHICH INTITIES THE

C. SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE

C. SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF TNET LEADS TO

C. HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

C. SUBUNIT: THE DEATH DOMAIN OF TRADD. WITH TRACTS SPECIFICALLY

C. WITH THE DEATH DOMAIN OF TRADD. TRATOUS TRADD-INTERACTING

C. WITH THE DEATH DOMAIN OF TRADD. THE FADD. THIS COMPLEX

C. THERI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

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BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD BROGER C., LOETSCHER H., LESSLAUER W.;

CELL 73:431-445(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1
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MEDLINE; 90110215.
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  GLYCOPROTEIN; REPEAT;
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EXTRACELLULAR (POTENTIAL POTENTIAL CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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NECROSIS FACTOR BINDING PROTEIN 1.
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Hererererere
                                                                                                                                                                                                         RX MEDLINE; 96011645.

RX SUTER B., PAULI U.H.;

RI GENE 163:263-266(1995).

CI -!- FUNCTION: RECEPTOR FOR THE ACTIVATED RECEPTOR. THE RESULTING COMPLEX (DISC)

CC RECRUITS CASCASE-B TO THE DETIVATED RECEPTOR. THE RESULTING COMPLEX (DISC)

CC RECRUITS CASCASE-B PROTECLYTIC ACTIVATION WHICH INITIATES THE CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APPOTOSIS (BY SIMILARITY).

CC PROTEASES) MEDIATING APPOTOSIS (BY SIMILARITY).

CC PROTEINS THE FINDING TO THE EXTRACELLULAR DOMAIN OF THEIL LEADS TO HOWOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS COMPLEX HOUSE THAT INTERACTS SPECIFICALLY COMPLEX BY THEIR ASSOCIATION WITH THE RECEPTORS DEATH DOMAIN OF TRADD. VARIOUS TRADD. ARE RECRUITED TO THEIR THE COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX BY SIGNALING (BY SIMILARITY: CONTAINS A LA-NGER/THER-TYPE CYSTEINE-RECRUITED TO SUBSCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC INFERENCE OF CONTAINS A LA-NGER/THER-TYPE CYSTEINE-RICH REGION.
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Best Local S
Matches 16
                                                                                             -1- SUBCELLULAR LOCATION: TYPE I ME
-1- SIMILARITY: CONTAINS A LA-NGFR/
EMBL; U1994; G1141753; -.

PROSITE; PS00652; TNFR_NGFR_1; 3.

PROSITE; PS50050; TNFR_NGFR_2; 2.

PROSITE; PS50017; DEATH_DOMAIN; 1.

PROSITE; PS50017; DEATH_DOMAIN; 1.

RECEPTOR; TRANSMEMBRANE; GLYCOPROTE
SIGNAL 1 21

POTENT
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P50555;
01-OCT-1996
01-OCT-1996
01-NOV-1997
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SUS SCROFA (PIG).
FUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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01-OCT-1996 (REL. 34,
01-NOV-1997 (REL. 35,
TUMOR NECROSIS FACTOR
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98.8%;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                            GLYCOPROTEIN;
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MISSING (IN REF. 4).
GPAA -> APP (IN REF.
GPAA -> CEOEAOGF CRC32;
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Pred. No. 0.00e+00;
1; Mismatches
TUMOR NECROSIS FACTOR RECEPTOR 1.
EXTRACELULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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MEDLINE; 91285014.

BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P.,

GRAY P.W., FELDMANN M., FOXWELL B.M.J.;

EUR. J. IMMUNOL. 21:1649-1656(1991).
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 91246188.
GOODWIN R.G., ANDERSON D., JERZY R.,
GOODBLAND N.G., JENKINS N.A., SMITH C.
COPELAND N.G., JENKINS N.A., COPELAND N.G., JENKINS N.A., SMITH C.
MOL. CELL. BIOL. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A., LEE
WONG G.H., CHEN E.Y., GOEDDEL
PROC. NATL. ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (REL.
01-MAY-1992 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNR1_MOUSE P25118;
     SEQUENCE FROM N.A.
TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA;
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123; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RODENTIA.
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larity 71.98;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REL. 22,
REL. 35,
REL. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
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TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
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TNFR-CYS 1.
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D.V.;
88:2830-2834(1991).
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                                                                                                                                                                                                                                                        DAVIS
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                                                                                                                             KISSONERGHIS A.M.,
                                                                                                                                                                                                                                                                                   BRANNAN C.I.,
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     RLIMONI. BUNDETHMANN F., GENTE R., LESSUADER W., STEINHEID R.,

MOL. HIMONOL. RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE FADD

CC -!- FUNCTION: RECEPTOR FOR THE ACTIVATED RECEPTOR. THE RESULTING

CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

CC PROTEASES, MEDIATING APOPTOSIS (ASPARTATE-SPECIFIC CYSTEINE

CC PROTEASES, MEDIATING APOPTOSIS (BY SIMILARITY).

CC -!- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THEIL LEADS TO

CC COMMONOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

CC PROVIDE A NOVEL MOLECULAR INTERPACE THAT INTERACTS SPECIFICALLY

CC PROTEINS SUCH AS TRAPS, RIP AND POSSIBLY FADD, ARE RECRUITED TO

CC THERI COMPLEX BY THEIR ASSOCIATION WITH THE COMPLEX

CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

CC I- SUBCCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SUBCCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CR EMBL; M59337; G202102; --

DR EMBL; M59337; G202102; JOINED.

DR EMBL; M5965; G202102; JOINED.

DR EMBL; M68667; G202102; JOINED.

DR EMBL; M68667; G202102; JOINED.

DR PIR; S16677; S16677.

DR PIR; S19021.

DR PIR; S19021.

DR PIR; S19021.
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[6]
SEQUENCE FROM N
MEDLINE; 931567
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DOMAIN
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MEDLINE; 94
BEBO B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
REPEAT
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MOL. I
-!- FU
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ROTHE J.G., BROCKHAUS M., GENTZ R.,
IMMUNOGENETICS 34:338-340(1991).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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MGD; MGI:98781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21:98781; TNFR1.
31:98781; TNFR1.
E; PS00652; TNFR_NGFR_1; 3.
E; PS50050; TNFR_NGFR_2; 3.
[E; PS50017; DEATH_DOMAIN; 1.
[The company of the c
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94245292.
., LINTHICUM D.S.;
NETICS 39:450-451(1994).
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BY SIMILARITY
POTENTIAL.
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CYTOPLASMIC (
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
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TNFR-CYS
POTENTIAL.
R -> G (I)
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Matches
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P22934;
01-AUG-1991 (REL. 19, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, RECEPTOR 1 PRECURSOR (P60)
    PROSITE; E
PROSITE; E
PROSITE; E
PROSITE; E
RECEPTOR;
SIGNAL
CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
TREPEAT
REPEAT
RE
                                                                                                                                                                                                                                                                                                                                                               LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
DNA CELL BIOL. 9:705-715(1990).

-i- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
REGRECATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

-i- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFAI LEADS TO
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTING
PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FAND, ARE RECRUITED TO
TOFIN COMPLEX BY THEIR ASSOCIATION WITH TRADD, THIS COMPLEX
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
HIT-TRADDS TO STORMATING OF STRADE THAT APOPTOSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LANTZ M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIMMLER A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                             NF-KAPPA B SIGNALING (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH
L; M63122; G207362; -.
; B36555; B36555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P19438; 1TNR.
TE; PS00652; TNFR_NGFR_1; 3.
TE; PS50050; TNFR_NGFR_2; 3.
TE; PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91090841
                                                                                                                                                                                                                     TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAURER-FOGY I., KROENKE M., SCHEURICH P.,
LSSON I., HAUPTMANN R., STRATOWA C., ADOLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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      CHÓRDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50129 MW;
                                                                                                                                                                                                     GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS POTENTIAL.
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Pred. No. 2.69e-225;
28; Mismatches 27;
    TNFR-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL)
4 X THER-CYS.
THER-CYS 1.
                                                                              TNFR-CYS 2.
                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                       TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4B6EEC09 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TNF-R1) (P55).
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G.R.;
                                                                                                                                                                                                                                                                                                                           REGION
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Best Local S
Matches 11
SEQUENCE OF 28-116.
MEDLINE; 72242988.
SAIRAM M.R., PAPKOFF
BIOCHEM. BIOPHYS. RES
[7]
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P01215;
21-JUL-1986 (REL. C
21-JUL-1986 (REL. C
21-JUL-1997 (REL. C
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                                                                                         SEQUENCE OF 28-116.
MEDLINE; 772436.
SAIRAM M.R., LI C.H.;
CAN. J. BIOCHEM. 55:755-760(1977).
                                                                                                                                                                    SEQUENCE OF 1-24.
MEDLINE; 81117268.
BIRKEN S., FETHERSTON J.,
J. BIOL. CHEM. 256:1816-1
                                                                                                                                                                                                                                                            SEQUENCE OF 1-98 FROM MEDLINE; 82267643. FIDDES J.C., GOODMAN F
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 94254248.
MIYOSHI I., KASAI N., HAYASHIZA
MIYOSHI I., KASAI N., HAYASHIZA
NIPPON RINSHO 52:940-947(1994).
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 80011660.
FIDDES J.C., GOODMAN H.M.;
NATURE 281:351-356(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN) EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
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                                                                                                                                                                                                                                                 MOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113;
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113; Conservative
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102
103
127
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       PAPKOFF H., Lt C...
                                                                                                                                                                                                                                              GOODMAN H.M.;
. GENET. 1:3-18(1981).
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                                                                                                                                                                    256:1816-1823(1981)
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01,
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66.1%;
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                                                                                                                                                                                                                                                                                          N.A.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                        HAYASHIZAKI
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                                                                                                                                                                                      CANFIELD
                               C.H.;
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Pred. No. 8.75e-221
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                 48:530-537(1972).
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                                                                                                                                                                                    70.ES.,
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                                                                                                                                                                                      BOIME
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RL EUR. J. BIOCHEM. 241:229-242 (1996).

CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLTROPIN AND GONADOTROPIN.

DR EMBL; J00152; G183319; JOINED.

REMBL; J00153; G183319; JOINED.

REMBL; J00154; G183319; JOINED.

DR EMBL; S70584; G546845; -.

DR EMBL; S70584; G546845; -.

DR EMBL; S70584; G546845; JOINED.

DR EMBL; V00485; G669156; -.

DR EMBL; V00485; G669156; -.

DR EMBL; V00487; G669156; JOINED.

DR PIR; A01481; THURAP.

DR PDB; 11RP; 01-NOV-94.

DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.

DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_2; 1.

DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 28-116.
MEDLINE; 74262937.
SHOME B., PARLOW A.F.;
J. CLIN. ENDOCRINGL. ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3.0 A MEDLINE; 94261179.
LAPTHORN A.J., HARRIS D.C., CANFIELD R.E., MACHIN K.J., NATURE 369:455-461(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE OF CARBOHYDRATES.
MEDLINE; 91122088.
WEISSHAAR G., HIYAMA J., RENWICK A.G.C.,
EUR. J. BIOCHEM. 195:257-268(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY ASSIGNMENT OF DISULFIDE MEDLINE; 81006887.
MISE T., BAHL O.P.;
J. BIOL. CHEM. 255:8516-8522(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE BEER T., VAN ZUYLEN C.W.E.M., LEEFLANK KAPTEIN R., KAMERLING J.P., VLIEGENTHART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 970
DE BEER T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BELLISARIO R.,
J. BIOL. CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 25-116
MEDLINE; 75211304.
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FUJIKI Y., RATHNAM P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 25-116. MEDLINE; 74011266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORGAN F.J., BIRKEN S., CANFIELD R.E.;
J. BIOL. CHEM. 250:5247-5258(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .T., WILLIAMS R.M., 37:1828-1828(1978).
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EM. 250:6735-6746(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARLSEN R.B., BAHL O.P.; 248:6796-6809(1973).
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624:428-435(1980).
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MORGAN F.J., IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BISHOP W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEEFLANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.F.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISAACS N.W.;
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P22762;
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HORMONE;
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01-OCT-1996
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                           RVTVMGGFKVENHTACHCSTCYYHK
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GOLOS T.G., DURNING M., FISHER J.M.;

DNA CELL BIOL. 10:367-380(1991).

-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

PIR; A39555.
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MACACA MULATTA (RHESUS MACAQUE).
MACACA MULATTA (RHESUS MACAQUE).
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 91321740
                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOPROTEIN HORMONES
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                               CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT
RVMVMGSVRVENHTECHCSTCYYHK 119
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                     CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259
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87; Conservative
                                                            Similarity 71; Conser
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(REL. 19, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANOTATION UPDATE)
N HORMONES ALPHA CHAIN PRECURSOR.
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larity 83.5%;
Conservative
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pred. No. 3.55e-149;
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BY SIMILARITY.
                                                           Score 552;
Pred. No. 3.
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CS -> SC (IN REF.
3BA19E2F CRC32;
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Best Local
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P01217;
21-JUL-1986 (REL. C
23-CCT-1986 (REL. C
01-NOV-1997 (REL. 3
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P07474;
01-APR-1988
01-APR-1988
01-OCT-1996
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CARBOHYD
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MEDLINE; 84024633.
ERWIN C., CROYLE M.L., DONELSON.
BIOCHEMISTRY 22:4856-4860(1983).
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J. PROTEIN CHEM. 3:143-156(1984).

-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCOPROTEIN
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                            BIOL.
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;ARYOTA; METAZOA; CHORDATA;
;HERIA; ARTIODACTYLA.
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A05096; A05096.
P01233; 1HRP.
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ACIDS RES.
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69; Conse
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83161058.
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                         THOMASON A.R., CSERBAK M.T., M. 258:4679-4682(1983).
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RES. 11:
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11:6873-6882(1983).
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76.7%;
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ALPHA CHAIN.
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LAST ANNOTATION UPDATE)
ALPHA CHAIN PRECURSOR.
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Pred. No. 8.57e-115;
Mismatches 15;
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                                                   MONCMAN C.L.,
                                                                                                                                                                                                                                                                                                                           NILSON
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                                                   WOYCHIK R.P.;
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P01218;
21-JUL-1986
01-APR-1990
01-OCT-1996
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CONFLICT
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J. BIOL.
                                                  OVIS ARIES (SHEEP).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; HORMONE; GLYCOPROTEIN; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUTROPIN, FOLLITROPIN AND (EMBL; X00003; E274391; -. EMBL; X00004; E274391; JOINED. EMBL; X00050; G607; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. BIOL. CHEM. 249:4166-4174(1974).

-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
SEQUENCE FROM N.A. MEDLINE; 90098887.
                                                                                                                        GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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PIR; A05132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUR. J.
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MEDLINE; 71111428.
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                                                                                                                                                                                                                                                                               RVTVMGGFKVENHTACHCSTCYYHKS
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L. CHEM. 246:866-872(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOCHEM.
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0 (REL. 14,
5 (REL. 34,
IN HORMONES
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EM. 246:850-865(1971).
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A05132.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                           STANDARD;
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21:489-497(1971).
                                                                                                                      01, CREATED)
14, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
ONES ALPHA CHAIN PRECURSOR.
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77.0%;
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Pred. No. 2.44e-115;
7; Mismatches 13;
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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Best Loc
Matches
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MEDIJINE; 72211144.

LIU W.-K., NAHM H.S., (
WARD D.N.;

WARD D.N.;

J. BIOL. CHEM. 247:435;
GIH1 10

GIH1_RAT

P11962; P70516;

01-OCT-1989 (REI

01-OCT-1989 (REI

01-NOV-1997 (REI
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DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
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SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS CHUNG D., SAIRAM M.R., LI C.H.; ARCH. BIOCHEM. BIOPHYS. 159:678-682(1973)
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91006170.
WEISSHAAR G., HIY!
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE
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MEDLINE; 82113052.
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                                                                                 94 TKATVMGNVRVENHTECHCSTCYYHKS 120
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                                                                                                                     34 GCPECKLKENKYFSKPDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF
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BL; X16977; G1366; -.
R; A01483; TTBOA.
R; A01484; UTSHA.
R; S06935; S06935.
R; S13200; S13200.
                                                                                                                                                         Local
                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                                   JINE; 910001/0.
SSHAAR G., HIYAMA J., RENWICK A.U.C.,
SCHAAR G., HIYAMA J., RENWICK A.U.C.,
J. BIOCHEM. 192:741-751(1990).
J. BIOCHEM. 192:741-751(1990).
SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                        NRVTVMGGFKVENHTACHCSTCYYHKS
                                                                                                            GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M M.R., PAPKOFF H.,
BIOCHEM. BIOPHYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E; 73190034.
M.R., PAPKOFF
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                                                                                                                                                Similarity
67; Conser
                                                                                                                                                                                                                                                                                                                 1215; 1HCN.
PS00779; GLYCO_HORMONE_ALPHA_1;
PS00780; GLYCO_HORMONE_ALPHA_2;
GLYCOPROTEIN; SIGNAL.
(REL.
(REL.
                                                                                                                                                                                     120
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                                                                                                                                                                                               197:535-539(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247:4351-4364(1972)
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                                    STANDARD;
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77.0%;
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CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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153:554-571(1972).
                                                                                                                                                                                     W.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred.
7; M
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E -> Q (IN
E -> Q (IN
CS -> SC (I
W; 13BA4DE1
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No. 2.
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Q (IN REF. 2)
Q (IN REF. 2)
SC (IN REF. 3
3A4DE1 CRC32;
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:ches 13;
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                                                                 GLHA_BALAC
P37036;
01-JUN-1994
01-JUN-1994
01-OCT-1996
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EMBL; V01252; G56580; -.

EMBL; V0257; G206111; -.

EMBL; M25243; G204470; -.

EMBL; M25544; G204471; -.

EMBL; M25544; G204471; -.
                                                                                                                                                                                                                                                                 CARBOHYD
CONFLICT
SEQUENCE
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CARBOHYD
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PROSITE;
HORMONE;
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                                                GLYCOPROTEIN CGA.
                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JT0408; TTRTA.
PIR; S27385; S27385.
HSSP; P01233; 1HRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY; TISSUE-PITUITAN MEDLINE; 82214055.
GODINE J.E., CHIN W.W., HABENER J.F.;
J. BIOL. CHEM. 257:8368-8371(1982).
                             BALAENOPTERA ACUTOROSTRATA EUKARYOTA; METAZOA; CHORDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-WISTAR-IMAMICHI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BURNSIDE
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  SEQUENCE
                    EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                               259
                                                                                                                                                                                     199
                                                                                                                                                                                                       34
                                                                                                                                                          94 TKATVMGNARVENHTDCHCSTCYYHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JENCE FROM N.A.
LINE; 89196918.
VSIDE J., BUCKLAND
E 70:67-74(1988).
                                                                                                                                                                                               GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKSF
                                                                                                                                               NRVTVMGGFKVENHTACHCSTCYYHKS
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                                                                                                                                                                                                                           Similarity 68; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EZASHI T., HIRAI
I. 7:877-885(1990)
                                                                                                                                                                                                                                                                                                                                                                          PS00779; GLYCO_HORMONE_ALPHA_1; PS00780; GLYCO_HORMONE_ALPHA_2; GLYCOPROTEIN; SIGNAL.
                     CETACEA
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(REL. 29,
(REL. 34,
N HORMONES
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larity 78.2%;
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.. 34, LAST ANNOTATION U
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AI T., KATO T.;
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                              (MINKE WHALE)
TA; VERTEBRATA;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                         Score 544; DB 1; L
Pred. No. 5.64e-114;
6; Mismatches 13;
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E -> Q (I
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5E507A0D CRC32;
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                                                                  ON UPDATE)
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                              (LESSER RORQUAL)
; TETRAPODA; MAMM
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CARBOHYD
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HORMONE;
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HSSP; PO1
PROSITE;
PROSITE;
PORONE;
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CARBOHYD
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BIOKHIMIIA 50:1972-1986(1985).
-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LOTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                               GODINE J.E., CHIN W.W., HABENER J.F.;
J. BIOL. CHEM. 257:8368-8371(1982).
-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, EVILITROPIN AND GONADOTROPIN.
EMBL; V01253; G56583; -.
EMBL; V01253; G56583; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLH2_RAT STANDARD; PRT; 120 AA. P11963; PT. 120 AA. 01-0CT-1989 (REL. 12, CREATED) 01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE) 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 82214055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOPROTEIN HORMONES ALPHA CHAIN 2
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
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                                                                                   y Match
34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSBATCCVAKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match
Local Similarity 70.1%;
les 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRVTVMGGFKVENHTACHCSTCYYHKS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKATVMGBARVZNHTZCHCSTCYYHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: PS00779; GLYCO_HORMONE_ALPHA_1; 1.
E: PS00780; GLYCO_HORMONE_ALPHA_2; 1.
E: GLYCOPROTEIN.
II 35 BY SIMILARITY
ID 14 64 BY SIMILARITY
ID 32 86 BY SIMILARITY
ID 36 88 BY SIMILARITY
ID 36 89 BY SIMILARITY
ID 63 91 BY SIMILARITY
ID 63 91 BY SIMILARITY
ID 56 56
IYD 56 56
IYD 82 82
OCE 96 AA; 10720 MW; E2CD30DF CRC
                                                                Similarity
67; Conser
                                                                                                                                                                                                                                                                                                                                                 PS00779; GLYCO_HORMONE_ALPHA_1; PS00780; GLYCO_HORMONE_ALPHA_2; GLYCOPROTEIN; SIGNAL.
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TR EMBL; W00852; G54799; -.

R EMBL; M22991; -; NOT_ANNOTATED_CDS.

R EMBL; M22992; G575520; -.

PIR; A01482; TIMSA.
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GORDON D.F., WOOD M.M., RIDGWAY E.C.,

GORDON D.F., WOOD M.M., RIDGWAY E.C.,

DNA 7:679-690(1988).

-i- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND

CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THY

CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THY
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SITE; PS00779; GLYCO_HORMONE_ALPHA_1;
SITE; PS00780; GLYCO_HORMONE_ALPHA_2;
CTYCOPROTEIN; SIGNAL.
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Pred. No. 1.
7; Mismatc
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A. 78:5329-5333(1981).
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SEQUENCE
                      GLHA_STRCA STANDARD; PRT; 96 AA. P80665; P00665; O1-OCT-1996 (REL. 34, CREATED) O1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) GLYCOPROTEIN HORMONES ALPHA CHAIN. STRUTHIO CAMELUS (OSTRICH). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETEUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY SEQUENCE OF 25-120. CLOSSET J., MAGHUIN-ROGISTER G., ENDOCRINOL. EXP. 8:164(1974).
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MEDLINE; 74075725.
MAGHUIN-ROGISTER G., COMBARNOUS Y.,
EUR. J. BIOCHEM. 39:255-263(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 89325834.
HIRAI T., TAKIKAWA H.,
MOL. CELL. ENDOCRINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; HORMONE; GLYCOPROTEIN; SIGNAL.
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) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                         CHORDATA; VERTEBRATA; TETRAPODA; AVES;
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63:209-217(1989).
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BY SIMILARITY.
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Pred. No. 1.98e-113;
7; Mismatches 13;
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MEDLINE; 97025333.

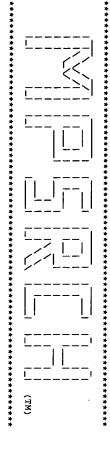
KOIDE Y., PAPKOFF H., KAWAUCHI H.;

EUR. J. BIOCHEM. 240:262-267(1996).

-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE
                                                                                                                                                                           SEQUENCE
                                           259
                                                                                     199
                                                               70
                                                                                               10 GCPECKLGENREFSKPGAPVYQCTGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKAF
                                                                                                                                                                                                                                                                         CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY LUTROPIN, FOLLITROPIN AND GONADOTROPIN. SITE; P$00779; GLYCO_HORWONE_ALPHA_1; 1. SITE; P$00780; GLYCO_HORWONE_ALPHA_2; 1.
                                                      TKITLKDNVKIENHTECHCSTCYYHKS
                                          NRVTVMGGFKVENHTACHCSTCYYHKS
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Pred. No. 1.30e-112;
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completed: Wed ne : 42 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Wed May 6 08:59:13 1998; MasPar time 14.96 Seconds 802.180 Million cell updates/sec

Description: Perfect Score:

Sequence: >US-08-804-166-6 (1-285) from US08804166.pep 2183 1 SRTSLLLAFGLLCLPWLQEG......GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150 Gap 11

Searched: 140555 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 41.694; Variance 64.494; scale 0.646

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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401 401	459	355	349	349	348	418	380	253	426	277	55	117	114	119	108	107	180	471	Length
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008727	Q62327	Q85308	860680	089118	Q85407	000275	000280	000276	014865	014866	Q62589	Q91119	Q91371	Q91370	Q90287	Q90286	Q95185	019131	ID
OSTEOPROTEGERIN.	TUMOR NECROSIS FACTOR	SECRETED RECEPTOR BIND	GARCIA-1966 RIGHT NEAR	SOMALIA-1977 RIGHT NEA	HOMOLOG OF VACCINIA VI	LYMPHOCYTE ASSOCIATED	LYMPHOCYTE ASSOCIATED	LYMPHOCYTE ASSOCIATED	DEATH RECEPTOR 3 BETA.	SOLUBLE DEATH RECEPTOR	ALPHA SUBUNIT OF GLYCO	GLYCOPROTEIN HORMONES	GONADOTROPHIN ALPHA 2	GONADOTROPHIN ALPHA 1	GONADOTROPIN ALPHA SUB	GONADOTROPIN ALPHA SUB	TUMOUR NECROSIS FACTOR	TUMOR NECROSIS FACTOR-	Description
2.84e-24 5.02e-22	1.00e-24	1.24e-25	1.52e-26	1.52e-26	1.52e-26	3.31e-34	3.31e-34	3.31e-34	1.12e-34	1.12e-34	2.97e-55	3.90e-80	5.78e-84	5.48e-85	1.68e-85	3.04e-85	1.42e-214	7.07e-219	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	17
142	143	146	147	150	155	154	159	160	160	167	167	173	179	178	180	180	181	181	181	181	181	181	187	TAT
6.5	6. 6	6.7	6.7	6.9	7.1	7.1	7.3	7.3	7.3	7.7	7.7	7.9	8.2	8.2	8.2		8.3			8. <sub>3</sub>		8. <sub>3</sub>		٥./
314	212	217	217					245		217				299		259	440	440	411	411	411	324 10	267	ALT TO
2 014293	4 007368	4 Q07369	4 Q07367		2 Q14407	2 014406	2 000220	2 014644	2 014643	2 Q16631	2 Q14405	_	2 Q16042	2 014798	2 092956	2 014755	2 014763	2 015531	2 014720	2 015508	2 015517	0 Q63199	4 002764	
PRC	SOMATOTROPIN 2 PRECURS	SOMATOTROPIN 3 PRECURS	SOMATOTROPIN 1 PRECURS	CELL SURFACE ANTIGEN O	CHORIONIC SOMATOMAMMOT	CHORIONIC SOMATOMAMMOT	CYTOTOXIC LIGAND TRAIL	PLACENTAL GROWTH HORMO	PLACENTAL GROWTH HORMO	SOMATOTROPIN PRECURSOR	SOMATOTROPIN PRECURSOR	RANK.	TUMOR NECROSIS FACTOR	CYTOTOXIC TRAIL RECEPT	HERPESVIRUS ENTRY MEDI	TRAIL RECEPTOR 3.	APOPTOSIS INDUCING REC	APOPTOSIS INDUCING PRO	DEATH RECEPTOR 5.	P53-REGULATED DNA DAMA	CYTOTOXIC TRAIL RECEPT	FAS ANTIGEN PRECURSOR.	OX40 PRECURSOR (FRAGME	OWTEOPROTEGERIN.
6.68e-11	4.19e-11	1.02e-11	6.39e-12	1.54e-12	1.41e-13	2.28e-13	.04e-	1.25e-14	1.25e-14	4.07e-16	4.07e-16	2.08e-17		1.71e-18	6.24e-19	6.24e-19	.77e-	.77e-	3.77e-19	3.77e-19	3.77e-19	3.77e-19	1.80e-20	7.34E-71

## ALIGNMENTS

AC DT	RES	Оy	ОУ	Qy Db	<b>% M O</b>	RP RC RA DR DR SQ	2000g	SE DE DE AC	RES
Q95185; 01-FEB-1997 (TREMBLREL. 02, CREATED) 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)	RESULT 2 ID Q95185 PRELIMINARY; PRT; 180 AA.	161 RODTICHCHMGFFLKGAKCISCHDCKNK-ECEKLCPTRPSTGKDSQDPGTT 210 : : :	101 SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCINCSLCPNGTVNIPCQE 160	41 ESPCPQGKYNHPONSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCL 100 :	Query Match 43.9%; Score 959; DB 4; Length 471; Best Local Similarity 66.7%; Pred. No. 7.07e-219; Matches 114; Conservative 28; Mismatches 28; Indels 1; Gaps 1;	SEQUENCE FROM N.A.  TISSUE-AORTA;  LEE EK., TALYOR M.J., KEHRLI M.E.;  SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.  EMBL; U90937; G2290398;  PROSITE; PS00652; TNFR_NGFR_1; 3.  SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;		O19131; 01-JAN-1998 (TREMBLREL. 05, CREATED) 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) TUMOR NECROSIS FACTOR-RECEPTOR I.	RESULT 1 ID 019131 PRELIMINARY; PRT; 471 AA.

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                                                           RESULT 4
ID Q90287
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ID Q90286
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Best Local Similarity 72.0%;
Matches 59; Conservative
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Best Local :
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  Q90287;
01-NOV-1996
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                            EMBL; D8
                                                                                                                                                                                                                                                                                                                                          O90286;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
60NADOTROPIN ALPHA SUBUNIT (FRAGMENT).
CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
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                                                                                                                                                                                                                                                                                   KOBAYASHI M., KATO Y., YOSHIURA Y., AIDA K.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; D86551; G1469836; -.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
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TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT)
                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                       KRVLV-NDVRLVNHTDCHCSTC
                                                                                                                                                     GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258
                                                                                                                                                                    GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKEV 86
                                                                                                          NRVTVMGGFKVENHTACHCSTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEKQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCRKEMYQVEISPCTVYRDTVCGCRKNQYRYYWSETHFQCLNCSLCLNGTVQISCKETQN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 43.2%;
Similarity 85.3%;
116; Conservative
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107 AA;
 (TREMBLREL.
(TREMBLREL.
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                                                           PRELIMINARY;
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11959 MW;
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CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                              107
                                                                                                                                                                                                 Score 453; DB 12;
Pred. No. 3.04e-85;
7; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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Pred. No. 1.42e-214;
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                                                            PRT;
                                                                                                                                                                                                                                                 880C6840 CRC32;
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Best Local S
Matches 5
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Best Local S
Matches 5
                  Q91371;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
GONADOTROPHIN ALPHA 2 SUBUNIT.
ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
                                                                                                                                                          LT 6
Q91371
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLEL. 05, LAST ANNOTATION UPDATE)
0CONADOTROPHIN ALPHA 1 SUBUNIT.
0CORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
EUKARYOTA; METAZOA; CHORDATA; YERTEBRATA; PISCES; GNATHOSTOMATA;
0STEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
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CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRA;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFO
[1]
                                                                                                                                                                                                                                                                                                                                                                                        GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., J. MOL. ENDOCRINOL. 11:265-273(1993).

EMBL; S69273; G546258; -.

PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.

PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.

SEQUENCE 119 AA; 13131 MW; ZEEF28F4 CRC32;
SEQUENCE FROM N.A.
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SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA
EMBL; D86552; G1469838; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
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                                                                                                                                                                                                                                                                            199
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                                                                                                                                                                                                                34 GCEECKLKENKLFSNPGAPVYQCTGCCFSRAYPTPLQSKKAMLVPKNITSEATCCVAKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 KRVLV-DDVKLVNHTDCHCSTC 108
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                                                                                                                                                                                                                                                                           GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258
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Similarity 72.0%;
59; Conservation
                                                                                                                                                                                                                                                                                                                                  h 20.7%;
Similarity 67.8%;
59; Conservative
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108 AA;
                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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12129 MW;
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Pred. No. 1.68e-85;
7; Mismatches 15
                                                                                                                                                                                                                                                                                                                                  Score 452; DB 12; Pred. No. 5.48e-85; 11; Mismatches 16;
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                                                                                                                                                          PRT;
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Matches 6
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CARBOHYD
CARBOHYD
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SIGNAL
CHAIN
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J. MOL. ENIDCRINOL. 11:265-273(1993).
EMBL; S69274; G546260; --
PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SEQUENCE 114 AA; 12519 MW; 473D3C83 CRC32;
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                        SUBMITTED (AUG-1997) TO -!- FUNCTION: INVOLVED 1
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-PITUITARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PITUITARY GLAND;
MEDLINE; 96020549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORONE SAXATILIS (STRIPED BASS)
EUKARYOTA; METAZOA; CHORDATA; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOPROTEIN HORMONES
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01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
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  258
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                                          199
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nes 67; Conser
                                                              33
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                                                                                                                                                                                                                                             SUBUNIT: HETERODIMER OF AN ALPHA AND A 1
L; L35071; G2322657; -.
SITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
SITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
                                                                                                                                                                                                                                                                                               SIMILARITY)
            YE-TEV-AGIKVRNHTDCHCSTCYFHK 116
                                                  GCEECTLRKNSVFSR-DRPVYQCMGCCFSRAYPTPLKAMKTMTIPKNITSEATCCVAKHS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTPLRSKQTMLVPKNITSEATCCVAKEGERVTTKDGFPVTNHTECHCSTCYYHKS 114
YNRVTVMGGFKVENHTACHCSTCYYHK
                                        GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GTH-ALPHA)
                                                                                  h 19.8%;
Similarity 65.5%;
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                        ENDOCRINOL. 15:23-35(1995).
                                                                                                                                                                                                                                       GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                 ELIZUR A., ZOHAR Y.;
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103
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AZOA; CHORDATA; ACTINOPTERYGII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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57
86
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                                                                                                                                                                                                                                                                                                      DEMBL/GENBANK/DDBJ DATA BANKS.
IN GAMETOGENESIS AND STEROIDOGENSIS
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01,
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                                                                                                                              MW.
                                                                                                                          GLYCOPROTEIN HORMONES A
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POTENTIAL.
W; CAFB9DOC CRC32;
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)

CHAIN PRECURSOR (GONADO
                                                                                   Score
Pred.
14; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 448; DB 12;
Pred. No. 5.78e-84;
                                                                                                                                                                                                                             BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PERCIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA;
                                                                                 re 433; DB 12; I
1. No. 3.90e-80;
Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GONADOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 114;
                                                                                                      Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNATHOSTOMATA
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Matches 4
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01-JAN-1998 (
01-JAN-1998 (
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
ALPHA SUBUNIT OF GLYCOPROTEIN HORMONES (FRAGMENT).
PHODOPUS SUNGORUS (STRIPED HAIRY FOOTED HANTER) (D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 8
Ω62589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; AF026071; G2570833; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALLES G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WARZOCHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; PRIMATES
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOLUBLE DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-PITUITARY;
MEDLINE; 96198779.
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les 57; Conserv
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   ENLFQC-FNCTLCLN-GTVH---
                                                       QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTPPPSL
                                                                                                                         DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDT
                                                                                                                                                                             TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               x90776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    026071; G2570833; -.
PS00652; TNFR_NGFR_1;
277 AA; 29111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K., RIBEIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6047 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           11.4%;
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                                                                                                                                                                                                                                                                                                                                                                           Score 249; DB 2;
Pred. No. 1.12e-34;
31; Mismatches 76
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred.
-LSCQEKONTVC-TCHAGFFLRENECVSCSNCKKSL
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06E165C7 CRC32
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1. No. 2.97e-55;
2. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 277;
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                                                                                                                     MAMMALIA;
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RESULT ID 0

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Best Local S
Matches 5
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Best Local Similarity
Matches 55; Conser
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01-JAN-1998
01-JAN-1998
01-JAN-1998
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01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
11-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
12-MPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
14-MPHOMO SAPIENS (HUMAN).
15-METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               UT 11
000276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (SEP-1997) TO EMBL/GE EMBL; AF026070; G2570831; -. PROSITE; PS00652; TNFR_NGFR_1; SEQUENCE 426 AA; 45950 MW;
                                                                                                                                                                                                                SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U94503; G2071953; -.
PROSITE; B800652; TIMFR.MGFR.1; 2.
SEQUENCE 253 AA; 26934 MW; A21C863E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
DEATH RECEPTOR 3 BETA.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. SCREATON G., XU X.
                                                                                                                                                                                                                                                                                                                          EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALLES G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                             129
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                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS :: | | | | | | | | | | | | ::
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                                                                                                        TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT
                                                                                                                            AALLLV---LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTPPPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT
                       QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                    DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S
                                                                            TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
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57; Conser
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                                                                                                                                                           11.3%;
larity 31.8%;
Conservative
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larity 31.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                  x. N.,
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                                                                                                                                                                                                                                                                                 OLSEN A., COWPER A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RENARD N.,
                                                                                                                                                           Score 247; DB 2; L
Pred. No. 3.31e-34;
31; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 249; DB 2;
Pred. No. 1.12e-34,
31; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
-LSCQEKQNTVC-TCHAGFFLRENECVSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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87E00821 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARLOT C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              253
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                                                                                                                                                                                                                                                                               TAN R., MCMICHAEL
                                                                                                                                                                                     Length 253
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 165
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ID 000275
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ID 000280
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Best Local S
Matches 5
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01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDAT
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPC
                                                                                                                                                                                                                                                                                                                                                                           000275;
01-JUL-1997 (TREMBLREL.
01-JUL-1997 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                 SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ
EMBL; U94502; G2071951; -.
PROSITE; PS00652; TWER_MCFR_1; 2.
SEQUENCE 418 AA; 45456 MW; 3D04954A CF
                                                                                                                                                                                                                                                                                                                                        LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; U94510; G2071967; -.. PROSITE; PS000652; TNFR_NGFR_1; 2. SEQUENCE 380 AA; 41192 MW; 17C92A14 CRC32;
                                                                                                                                                                                                                                                                        BELL J.;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SCREATON G., XU X.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BELL J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SCREATON G., XU X.N.,
                                                                                                                                                                                                                                                                                                                           EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ENLFQC-FNCTLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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Local Similarity 31.8%;
hes 55; Conservative
                                                                                                                        62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT
                                                   DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQVRHYW-S
                                                                              TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCRPGWFVECQVS 128
                                                                                                        TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS
ENLFQC-FNCTLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCS
                         QCVSSSPFYCOPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                            h 11.3%;
Similarity 31.8%;
55; Conservative
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                                                                                                                                                                                                                                                                                                                                        CHORDATA; VERTEBRATA;
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                                                                                                                                                                                                                                                                                   OLSEN A.,
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04, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
                                                                                                                                                            Score 247; DB 2; Le
Pred. No. 3.31e-34;
31; Mismatches 72;
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Pred. No. 3.31e-34;
31; Mismatches 72;
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3D04954A CRC32;
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RESULT
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ID Q85407
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                                                                                                                 Query Match 9.8%;
Best Local Similarity 38.5%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.8%;
Best Local Similarity 38.5%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BANGLADESH-1975;
MEDLINE; 94088747.
MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;
NATURE 366:748-751(1993).
EMBL; L22579; G439102; -
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 15
Q89118
                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SOMALIA-1977;
MASSUNG R.E., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,
TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U1841; G88585; ---
PROSITE; PS00652; TNFR_NGFR_1; 2.
SEQUENCE 349 AA; 38272 MW; OFDCC784 CRC32;
                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
SOMALIA-1977 RIGHT NEAR-TERMINAL REGION.
VARIOLA VIRUS.
VARIOLA VIRUS.
VIRIDAE; DS-ONA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                               Q89118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q85407;
01-NOV-1996 (TREMBLREL. 01, CREATED
01-NOV-1996 (TREMBLREL. 01, LAST SE
01-JAN-1998 (TREMBLREL. 05, LAST AN
HOMOLOG OF VACCINIA VIRUS CDS B28R.
                                                                                                                                                                                                                                                                                                                    ORTHOPOXVIRUSES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIOLA VIRUS.
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
 97
                                                        37 NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI 96
                                                                           40 HNLCCLSCPPGTYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET 97
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                            98 RSCNTTHNRICECSPGYY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSCTVDRDTVCGCRKNOY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNLCCLSCPPGTYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSCNTTHNRICECSPGYY 114
SSCTVDRDTVCGCRKNQY 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
                                                                                                                   Score 214; DB 11;
Pred. No. 1.52e-26;
14; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 214; DB 11; Pred. No. 1.52e-26; 14; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AA.
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                                                                                                                                                Length 349;
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Search completed: Wed May Job time: 72 secs.

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Kelease 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Wed May 6 14:22:01 1998; MasPar time 1326.51 Seconds 1499.916 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: >US-08-804-166-7
(1-1301) from US08804166.seq
1301
1 CTCGAGATGGCTACAGGTAA......CACAATAAGGATCCCTCGAG 1301
GAGCTCTACCGATGTCCATT......GTGTTATTCCTAGGGAGCTC

Nmatch Scoring table: STD: TABLE default Gap 6 Dbase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

emb153
1:em\_in 2:em\_or 3:em\_om 4:em\_ov 5:em\_pl 6:em\_htg
1:em\_hum1 8:em\_hum2 9:em\_ba 10:em\_ro 11:em\_un 12:em\_vi
13:em\_pat
genbank105
14:gb\_ro 15:gb\_om 16:gb\_ov 17:gb\_in 18:gb\_pl 19:gb\_ba
20:gb\_st 21:gb\_v1 22:gb\_ph 23:gb\_sy 24:gb\_un 25:gb\_pat
26:gb\_htg 27:gb\_pr1 28:gb\_pr2

Database:

Database:

Statistics: Mean 11.236; Variance 5.267; scale 2.134

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result No. 1 1 2 3 4 4 5 5 6	<b>J</b>	æ	o	10	11	12	13	14
Sid 514 514 514 514 514	514	514	514	514	514	514	514	514
Watch 39.5 39.5 39.5 39.5 39.5 39.5		39.5	39.5	39.5	39.5	39.5	39.5	39.5
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H.sapiens mRNA for TNF Synthetic DNA for TNF- Human tumor necrosis f TNF alpha gene. Sequence 24 from paten Human tumor necrosis f cDNA for (55kD TNF-BP) Homo sapiens tumor nec	COND FOR (SEED THEFTED)	Homo sapiens tumor nec	Human tumor necrosis f	H.sapiens TNF-R mRNA f	Sequence 1 from Patent	Sequence 1 from patent	Synthetic nucleotide s	Sequence 2 from patent
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1 (bases 1 to 1368)
Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stratowa, C.
TNF-receptor, TNF-binding protein and DNA coding therefor
Patent: EP 0393438-A 48 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
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Gray, P.W., Barrett, K.J., Chantry, D., Turner, M. and Feldman, M. Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
9,1017509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Draft entry and computer-readable sequence for [Proc. Sci. U.S.A. (1990) In press] kindly submitted by P.W.Gray, 13-AUG-1990.
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TNF receptor; transmembrane receptor; tumor necrosis factor
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FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTEKGGLLEGTTTFKPLAPNRSFSPT
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Schall.T.J., Lewis.M., Koller,K.J., Lee,A.L., Rice,G.C., Won Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and Goeddan
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/db_xref="pid:g339745"
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FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTRFDAPNPSFSPT
PGFTPTLGFSPVPSSTTTSSSTYTPGDCPNFAAPRRVAPPYQGADPILATALASDPI
PNPLLKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELON
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1. .2087
                                                                                                                                                                                                                                                              /note="tumor necrosis factor receptor"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                   TNF-binding proteins
Patent: EP 0417563-A
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Brockhaus, M., Dembic, Z.,
Schlaeger, E.J.
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                                                  /product="15 kD TNF-BP"
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PGFTPFLGFSPVPSSTFTSSSTYTPGDCPNFAAPRRETARPXQADPILATALASDPI
PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLKWKEFVRRLGLSDHEIDNELGN
PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPRLWKEFVRRLGLSDHEIDNELGN
                                         GRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPP#
                                                                                                                                                                                                                 /organism="Artificial
187. .1554
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Loetscher, H.

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Loetscher, H., Pan, Y.-C.E., Lahm, H.-W., Gentz, R., Brockha
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Cell 61, 351-359
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                                                                                /organism="Homo sapiens"
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187. .273
                                                 /product="tumor necrosis 187. .1554
                                                                                                                                            Location/Qualifiers
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                                                                      /gene="INF receptor"
                          /note="55 kDa
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         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H. (bases 1 to 2112)
Himmler, A., Maurer-Fogy, I., Kroenke, M., Scheurich, P.,
                                              Homo sapiens
                                                                     tumor necrosis factor receptor
                                                                                            M63121 M75861
                                                                                                                   Human tumor necrosis
                                                          Human cDNA to mRNA.
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704 666 644 606 584 546 524 486 464

factor receptor (TNF receptor) mRNA, complete

30-SEP-1991

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PSLLR"
                                                                                                       /db_xref="PID:g339754"
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GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
                                                                          h 39.5%;
Similarity 100.0%;
514; Conservative
                                                                                                                                                                                                      /gene="TNF receptor"
/product="tumor necrosis factor receptor"
629 c 587 g 450 t
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274. .1551
                                                                                                                                                                         receptor"
                                                                                   Score 514; DB 27;
Pred. No. 0.00e+00;
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                                                                                                                 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                                                                                                     AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 566
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AATGTTAAGGGCACTGAGGACTCAGGCACCACAG
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Molecular cloning and expression of human and rat t factor receptor chain (p60) and its soluble derivat necrosis factor-binding protein DNA cell Biol. 9, 705-715 (1990)
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FFGLCLLSLEFGLMYRYQRMKSKLYSIVCGKSTPEKGELBGTTTKKLAPNPSFSTF
PGFTPTLGFSFVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYGGADFILATALASDFI
PNPLCKWEDSAHKFQSLDTDDPATLYAVVENVPPLRWKETVRRLGLSDHEIDRLELQN
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294. .1571
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/product="tumor necrosis factor receptor"
/ 632 c 589 g 456 t
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/db_xref="taxon:9606"
207. .293
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207. .1574
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Pred. No. 0.00e+00;
^ Mismatches 0;
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                                                                                                                  345 GATAGTGTGTGCCCCAAGGAAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 404
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TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACACTGCCTC
                                    AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                           AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
                                                                                                                                                                                             39.5%;
1 Similarity 100.0%;
514; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R., Aderka,D., Holtmann,H. and Wallach,D. Soluble forms of tumor necrosis factor receptors (TNF-Re). The for the type I TNF-R, cloned using amino acid sequence data of soluble form, encodes both the cell surface and a soluble form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1. x55313
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 2161)
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2161
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PNPLKWEDSAHKPGSLDTDDPATLYAVVENVPLRWEEFVRLGLSDHEIDRLEIGN
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2145. .2150
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757. .857
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634. .756
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/gene="TNF-R"
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/db_xref="taxon:9606"
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Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
Proteases capable of shedding the soluble TNF-receptor a
derived peptides and antibodies against the proteases in
the shedding.....
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Other publication ZA 9407962
Other publication JP 7194376
Other publication AU 7574294
Other publication CA 2133872
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                                                                           /organism="unidentified"
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KQNTYCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTYLLPLVI
FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNFSSPT
PGFTPFTIGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYGGAPFLAFALSDPI
PNPLOKWEDSAHKPGSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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Unclassified.

3 1 (bases 1 to 2175)

S Wallach,D., Brakebusch,C., Varfolomeev,E. and Molecules influencing the shedding of the TN preparation and their use preparation and their use preparation and their use 1. Coation/Qualifiers

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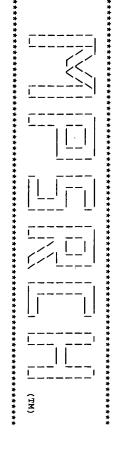
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Location/Qualifiers
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Search completed: Wed May Job time: 1340 secs. σ 14:44:21 1998

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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 15:05:10 1998; MasPar time 167.20 Seconds 897.906 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: N.A. Sequence: (1-1301) from US08804166.seq >US-08-804-166-7

Comp: 1 CTCGAGATGGCTACAGGTAA......CACAATAAGGATCCCTCGAG 1301 GAGCTCTACCGATGTCCATT......GTGTTATTCCTAGGGAGCTC

Scoring table: TABLE default Gap 6

Nmatch STD Dbase 0; Query 0

Searched 159651 seqs, 57698962 bases x

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.269; Variance 5.321; scale 1.742

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	514	39.5	1334	ㅁ :	Q06282	Plasmid Tumour Necros	0.00e+00
N	514	39.5	1368	œ	Q49932	Lambda-derived TNF-R	0.00e+00
ω	514	39.5	2062	4	Q24440	Encodes TNF-alpha 55k	0.00e+00
4	514	39.5	2062	ω	Q20973	TNF-alpha binding pro	0.00e+00
G	514	39.5	2088	ν	Q10883	30kD TNF inhibitor pr	0.00e+00
σ	514	39.5	2111	N	Q10955	Encodes human 55kD TN	0.00e+00
7	514	39.5	2175	15	Q90513	p55 TNF-R gene.	0.00e+00
8	514	39.5	6889	18	T15931	DHFR/intron (WTrasSD)	0.00e+00
9	512	39.4	2141	ب	Q06285	Human Tumour Necrosis	0.00e+00
10	512	39.4	2176	N	Q12215	Type I TNF receptor.	0.00e+00
11	510	39.2	2170	Q	Q50870	p55 Tumour necrosis f	0.00e+00
12	478	36.7	803	4	Q24441	Encodes truncated INF	0.00e+00
13	416	32.0	579	ω	Q14800	Human chorionic gonad	6.61e-279
14	415	31.9	836	17	T03212	Single chain gonadotr	3.64e-278
15	415	31.9	836	17	T03243	Single chain gonadotr	3.64e-278

Query Match

39.5%;

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## ALIGNMENTS

HE SUPPLIES OF SUP DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanismsm to TNF action Disclosure; Fig 1(1-3); 51pp; German.

S Disclosure; Fig 1(1-3); 51pp; German.

C pTNF-BP15 is one of 30 positives clones in a screened cDNA library from induced TNF-induced fibrosarcoma cells. A TNF-BP had been isolated from the urine of patients with uraemia and probes/primers were constructed from the determined amino acid sequence.

To produce a vector expressing a soluble form of TNF-binding protein, this plasmid was cut with Xmm1, amplified by PCR and the amplified DNA cut with Banmil and EcoRI.

The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19 (BRL) cut with Banme enzymes to recover pTNF-BP. This was cut with Banmil and EcoRI, and the recovered fragment inserted into pAD-CMV1 (Q06283) to give the required plasmid pADTNF-BP.

See also Q06282-Q06285. pAD-CMV1 See also Sequence 24-OCT-1990.
06-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT.
Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa WPI; 90-321987/43. Q06282 standard; DNA; 1334 BP. Q06282; Plasmid Tumour Necrosis Factor Tumour necrosis factor binding pTNF-EP15; ss. Homo sapiens. P-PSDB; R07449 /product=TNF-BP EP-393438-A. 29-JAN-1991 (first entry) /\*tag= BP; Location/Qualifiers 213..1325 299 Factor-Binding Protein 15 cDNA insert. pinding protein; TNF-BP; TNF-receptor; ? 409 C; 342 G; ü 284 T;

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30-MAR-1992; US-860710.
(IMMY) IMMUNEX CORP.
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049932 standard; cDNA to mRNA; 1368 BP.
049932;
29-APR-1994 (first entry)
Lambda-derived TNF-R cDNA.
Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
graft verses host disease; sepsis; inflammation; allergy;
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New fusion protein tumour necrosis factor and human receptor - useful in therapy, diagnosis and assays crheumatoid arthritis, diabetes, cerebral malaria, se Disclosure; Page 57-59; 85pp; English.
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P-PSDB; R42059.
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RESULT 3

ID Q4440;

AC Q24440;

AC Q24440;

DT 05-NOV-1992 (first entry)

DE Encodes TNF-alpha 55kD receptor.

E tumour necrosis factor alpha; extracellular binding domain;

KW treatment; pulmonary diseases; septic shock; HIV infection;

KW malaria; viral meningits; graft versus host disease;

KW autoimmune disease; rheumatoid arthritis.

CS Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or II-1, particularly in conditions in which both TNF and II-1 play a causitive role. They may be used to treat cachaxia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and autoimmune dysfunctions.

Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in Q49931-32 encode human tumour necrosis receptor (TMF-R) and the sequences in Q4993-34 encode human interleukin-1 receptor (II-IR). These sequences were used in production of a fusion protein which conformed to one of the formulae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNF-R-linker-TNF-R-linker-IL-1R
IL-1R-linker-TNF-R-linker-TNF-R
TNF-R-linker-TNF-R
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l Similarity 100.0%;
514; Conservative
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Pred. No. 0.
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/\*tag= a /product= hu mat\_peptide

human

TNF-alpha 1265..1267

Location/Qualifiers 156..1517

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first three cysteine-rich subdomains of TNF alpha receptor for

treating autoimmune disease, septic shock, HIV etc.

Claim 4; Fig 1; 43pp; English.

This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA

Library in gt10 was screened with probe Q29236. Ten hybridising clones

were plaque purified and cDNA size determined by PAGE against an

Eco RI digested phage DNA. The inserts of two cDNA clones were then

sequenced. The coding region of the majority of the human TNF-alpha

SkD receptor was isolated as an EcoRI fragment encoding 374 amino

Cacids, and cloned into a mammalian cell expression vector, resulting

in prNFR. A derivative of the TNF-alpha receptor was produced by

censineering a termination codon just prior to the transmembrane

commain. PCR with primers Q29237,8 generated a 300bp

restriction fragment which was cloned into prTNFR, giving pTNFRecd.

DNA sequencing confirmed this contained the designed DNA sequence.

The TNF-alpha receptor expression plasmids were then transfected

sensets Confirmed this contained the designed DNA sequence.
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Best Local Similarity 100.0%;
Matches 514; Conservative
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18-OCT-1991; G01826.
18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS SI
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mat_peptide 1433..1435
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WPI; 92-167156/20.
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/codon= Seq:"GAC", aa:As
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mat_peptide 1258..1260
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ttccagttgcttcaattgcagcctctgcctcaatgggaccgttgcaccttctcctgccaggag
                                            TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC
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M, Gray PW, Turner
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Pred. No. 0.00e+00;
0; Mismatches 0
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Q20973;
                                                                                                                                                                                                                                                                                                                                                   e.g. rheumatoid arthritis
Disclosure; Fig 1; 25pp; English.
The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obtd. from a human placental cDNA library in lambda gtl1 using a probe (Q20974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is useful for treating diseases where TNF alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases, specifically rheumatoid arthritis. See also Q20974.

Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "encodes the TNF alpha receptor" GB2246569-A.
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15-JUN-1990; GB-013410.
(CHAR-) CHARING CROSS S
Feldman M, Gray P, Turr
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Tumour necrosis factor alpha; a
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Similarity 100.0%;
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N AU9058976.
PR 16-JUL-1990; 058976.
PR 16-JUL-1990; US-450329.
PR 11-DEC-1989; US-450329.
PR 11-DEC-1989; US-450329.
PR 07-FEB-1990; US-479661.
PR 07-FEB-1990; US-479661.
PR 07-FEB-1990; US-479661.
PR 07-FEB-1990; US-479661.
PR 11-DEC-1989; E10986.
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha P-PSDB; R10986.
PT Tumour becas, useful as therapeutic agent.
PT and -beta, useful as therapeutic agent.
PT the sequence was obtd. was isolated from a cDNA library and composition of TNF whole CC prepci. from RNA form U937 cells treated with PMA/PHA. The whole CC inhibitor for use in the treatment of inflammatory and degenerative
                                                                                                                                                Query Match
Best Local S
Matches 51
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CDS
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See also Q10878, Q10884 and Q10907
Sequence 2088 BP; 439 A; 6
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30kD TNF inhibitor precursor gene :
Tumour necrosis factor; inhibitor;
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                                                          aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 408
                                                                                             GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404
                                                                                                            gatagtgtgtgtccccaaggaaaatatatccacctcaaaataattcgattttgctgtacc 348
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           tycagygagtytyagagcygctccttcaccycttcagaaaaccacctcagacactycctc
                                               AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC
                                                                                                                                              39.5%;
| Similarity 100.0%;
| 514; Conservative
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08-MAR-1990; CH-000746.
20-APR-1990; CH-001347.
(HOFF ) HOFFMANN-LA ROCHI
Brockhaus M, Dembic Z, Ge
                                                                                               prodn.
Claim 4; Fig 1; 26pp; German.
Claim 4; Fig 1; 26pp; German.
Partial amino acid sequences were determined for the 55 and 75kD
Partial amino acid sequences were determined primers were
synthesised based on these partial sequences. The primers were used
to produce a cDNA fragment for use as aprobe to screen a human
placental cDNA bank constructed in lambda gtll. Positive clones were
identified and sequenced. DNA constructs comprising the TNT-BP coding
sequence may also contain a fragment encoding a human Ig domain.
Recombinant constructs are used to transform cells to confer
improved TNF-binding properties.
See also Q10956.
Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T;
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EP-417563-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
/*tag= a
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                                                                                                                                                                                                                                                                 encoding them, useful
                                                                                                                                                                                                                                                                  Insoluble tumour necrosis factor binding proteins - encoding them, useful in pharmaceutical prods. and :
                                                                                                                                                                                                                                                                                           WPI; 91-081851/12.
P-PSDB; R11082.
                                                                                                                                                                                                                                                                                                                    Brockhaus M,
Schlaeger EJ;
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31-AUG-1990;
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/*tag= b
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                                                7 Match 39.5%;
Local Similarity 100.0%;
les 514; Conservative
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              gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 366
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Z, Gentz R, Lesslauer
                                               Score 514;
Pred. No. 0.
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Mismatches 0;
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PT New protease capable of cleaving soluble tumour necrosis factor PT (TNF) receptor - from cell-bound TNF- receptor, useful for antagonising deleterious effects of TNF.

PT antagonising deleterious effects of TNF.

CC Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different candiding agents, e.g. phorbol myristate acetate (PMA), depending on cell canding agents, e.g. phorbol myristate acetate (PMA), depending on cell candiding response is the spacer region (see RF5012) in the extracellular commain. This region is located close to a site of cleavage of the collecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras complete that are represented by R75007-11. This spacer region was subjected to deletion mutations (R75013-25) and substitutions
                                                                                                                                                                                    12-OCT-1993; IL-107268.

(YEDA ) YEDA RES & DEV CO L

Batkin M, Brakebusch C, V

WPF; 95-194342/26.

P-PSDB; R75084.
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/product= p:
misc_signal
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Q90513
Q90513;
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11-OCT-1994; 075742
12-OCT-1993; IL-107:
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T15931 standard; I
T15931;
20-JUN-1996 (fir
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Improved process for the expressing high level of cells contg. a DNA constr
                                                                                                                              28-JUL-1995; U09576.
05-AUG-1994; US-286740.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                    Synthetic.
WO9604391-A1.
                                                                                                                                                                                                                                                                                  DHFR/Intron (WTrasSD)-TnFr-IgG dicistronic vector.
Recombinant host cell; dihydrofolate reductase; selectable n
DHFR; ras splice donor; dicistronic vector; gene expression;
immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
                                                                             Crowley CW;
WPI; 96-129407/13.
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PR 21-APR-1989; DE-913101.
PR 21-JUN-1989; DE-920282.
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Matches 514; Conservative
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pools).
Sequence
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A dicistronic vector (715930) comprises a regulatory region derived from the cytomegalovirus immediate-early gene, a selectable dihydrofolate reductase gene positioned within an intron having a 5' wild-type ras splice donor site, a downstream sequence coding for an immunoadhesin, TnFr-IgG, capable of binding tumour necrosis factor, and a poly-A sequence. Transfection of CHO DHFR- cells and subsequent methotrexate amplification and growth of the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5 ug/ml (15-fold higher compared to conventional vector amplified
                                                                                                                                                      Q06285 standard; DNA; 2141 BP.
Q06285;
Q06285;
Q9-JAN-1991 (first entry)
Human Tumour Necrosis Factor-Receptor cDNA insert
Tumour necrosis factor binding protein; TNF-BP; TN
lambdaTNF-R2; raTNF-R8; ss.
Homo sapiens.
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raTNF-R8 (Q06284) was used to screen the HS913T cDNA 11
LambdaTNF-R2 encodes the complete human TNF-R2 and was construct a plasmid (pADTNF-R) expressing the product t as pADTNF-BP (see Q06282).

See also Q06282-Q06285.

Sequence 2141 BP; 455 A; 633 C; 593 G; 46
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Q12215;
                                                                                                                                                                                                                                                                                  12-SEP-1991 (first
Type I TNF receptor
Tumour Necrosis Fact
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P-PSDB; R07451.
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                                                                                                                                                                                                                                                                                                                                                                   standard;
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Similarity 99.8%;
513; Conservative
                                                                                                  I TNF receptor 256..318
                                                                                                                                                                                                                       Location/Qualifiers 244..246
                                                                                                                                                            termination
256..1620
                                                                                                                                                                                                                                                                                    Factor; TNF; binding
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13-DEC-1990; 1124133.
13-DEC-1989; IL-092697.
12-JUL-1990; IL-095064.
(YEDA) YEDA RES 6 DEV CO L'
Wallach D, Nophar Y, Kemper
Aderka D;
WPI; 91-186774/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                  /number= 4
polyA_signal
/*tag= m
EP-433900-A.
                                                                                                                                                                                                                                      Recombinant tumour necrosis factor binding protein I - prepd. by transfecting eukaryotic cells with vector contg. deoxyribonucleic acid encoding human type T TNF receptor or soluble domain Disclosure; Fig 1(D); 30pp; English.

The Tumour Necrosis Factor Binding Protein I is the soluble form of type I TNF-receptor and constitutes a fragment of the cell surface form of this receptor, corresp. to its extracellular domain. There is no characteristic poly(A) addition signal near the 3' end of the cDNA. The sequence ACTAAA (tag m) may serve as an alternative to this signal, but with low efficiency.
                                                                                                                                                                                                                              of the cDNA. The sequence A alternative to this signal, See also Q12212-15.
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/label= transmembrane_domain
/label= init 385..504
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                                                         tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc
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larity 99.8%;
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Pred. No. 0.00e+00;
0; Mismatches 1
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Matches 51
                                                                                                                                                                                                                                                                                     disease, septic shock, etc.

Claim 2; Figure 1; 17pp; English.

Modification of the tumour necrosis factor receptor by mutation deletion modulates signal transduction and/or cleavage effected the receptor. This modulation of activity can also be achieved using effector proteins which interact with the TNF receptor.

Molecules which interact with the TNF receptor or the effector proteins can be used to treat or prevent diseases associated wit TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft rejection; graft vs. host disease or septic shock. They can also be used to treat overdoses of exogenous TNF.

Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      p55 Tumour necrosis factor receptor coding sequence.
TNF; tumour necrosis factor; receptor; disease; autoimmunity; rheumatoid arthritis; graft rejection; graft vs. host; septic effector protein; ss.
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                                      aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac
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                                                                                                                       Similarity 512; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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larity 99.6%;
Conservative
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Pred. No. 0.00e+00;
0; Mismatches 2
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Best Local Similarity 99.8%;
Matches 479; Conservative
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18-OCT-1990; GB-022648.

(CHAR-) CHARING CROSS SI

Brennan FM, Feldmann M,

WPI; 92-167156/20.
                                                                                                                                                                                                                                                                                                                                                                                                                   first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.

Example: Fig 7; 43pp; English.

This sequence encodes the designed TNF-alpha 55kD receptor derivative, as present in purfeced. This was produced as described 024441. This derivative lacks the 81 carboxyl terminal residues of the cytoplasmic domain. The derivative could be used in the regulation of TNF-alpha mediated responses by binding and sequestering human TNF-alpha eg. in the treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis, graft versus host disease and autoimmune diseases, esp. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encodes truncated TNF-alpha 55kD receptor (197 amino acids). tumour necrosis factor alpha; extracellular binding domain; treatment; pulmonary diseases; septic shock; HIV infection; malaria; viral meningits; graft versus host disease; autoimmune disease; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                            arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide capable of binding human TNF alpha first three cysteine-rich subdomains of TNF alpha r
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30-APR-1992.
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07-MAY-1991; U03162.
08-MAY-1990; US-520703
(UYNE-) UNIV MED NEW J
Campbell RK, Moyle WR;
WPI; 91-353528/48.
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mat_peptide
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sig_peptide
/*tag= c
                                              New glyco-protein hormone analogues - for inducing fertility as immuno-castration agents, for suppressing reproductive system development and as immuno-contragestive vaccines.

Example 3; Fig 4a; 94pp; English.

The sequence is an analogue of hCG beta subunit cDNA contg. two silent mutations which eliminate restriction sites. It was prepd. from the plasmid pRMB-hCG-beta, a construct contg. the hCG beta subunit isolated from human placenta (Fiddes and Goodman) in plasmid pRMB, a derivative of pCCB designed to facilitate cloning of glycoprotein hormones. The sequence was used as the starting construct for many mutants. (See R15061-R15125 and R15161-R15198). Sequence 579 BP; 128 A; 205 C; 151 G; 95 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1992 (first entry)
Human chorionic gonadotropin beta :
Glycoprotein hormone; hCGB; ferti
immuno-contragestive; vaccine; ds.
                                                                                                                                                                                                                                                                                                                 mutation
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11-FEB-1992
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W09116922-A.
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              Similarity
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   Conservative
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              32.0%;
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Score 416; DB 3; Le
Pred. No. 6.61e-279;
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                        Length
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   Gaps
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104

ccacggtgccgcccatcaatgccaccctggctgtggagaaggagggctgccccgtgtgc 163

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RESULT FIRST                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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P-PSDB; R86247.

Methods for altering fertility in mammals, esp. humans - e.g. Methods for altering fertility by reducing the activity and/or levels of stimulating fertility by reducing the activity and/or levels of circulating glyco:protein hormones having lutropin activity Example 12; Fig 6; 102pp; English.

Analogue 1 (human CG-beta(1-145)-linker-human CG-alpha(1-92)) is a specific example of a single chain gonadotropin having a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a CG alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1996 (first entry)
Single chain gonadotropin analogue 1 coding sequence.
Single chain gonadotropin; human chorionic gonadotropin;
Single chain gonadotropin; human chorionic gonadotropin;
alpha; beta; subunit; analogue; glycoprotein hormone; fer
inhibit; stimulate; increase; lutropin; luteinising hormo
follicle stimulating hormone; FSH; vaccine; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "single-strand overhang.
strand also has a single-strand
its 5'-end; the sequence of the
5'-TCCGGATTAGCTTGAGATGGATCC-3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note "nucleotides 93..527 encode aminual 1-145 of hCG beta-subunit; nucleotides 528..551 encode a (Gly-Ser)4 linker and nucleotides 552..827 encode amino acids 1-92 of gonadotropin alpha-subunit"
                                                                                                                                                                                                                                                                                                                                                              W09522340-A1.
24-AUG-1995.
17-FEB-1995; U02067.
18-FEB-1994; US-199382.
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33..92
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                                                                                                                                                                                                                                                                                                                                       subunit at the C-terminus, joined by a linker of 1-16 amin The analogue has lutelnising hormone (lutropin) activity a useful for inducing ovulation and increasing training the sequences coding for analogue 1 were cloned from a hum placental cDNA library using strand overlap extension PCR. Sequence 836 BP; 166 A; 282 C; 222 G; 166 T;
 1230
                                                                                                                             1050
                     471
                                                                                                      351
                                                                                                                                                                    990
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                                                                                                                                                                                                                                                        CCACGGTGCCGCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC
                                                                                                                                                                   GGGGTCCTGCCGGCCCTCCAGGTGGTGCAACTACCGCGATGTGCGCTTCGAGTCC
                                                                                                                                                                                                             ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG
                                                                                  416;
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Reproper Repropersion of the activity and/or levels of stimulating fertility by reducing the activity and/or levels of stimulating fertility by reducing the activity and/or levels of circulating glyco:protein hormones having lutropin activity example 23; Fig 18: 102pp; English.

Analogue la (human CG-beta(1-145)-linker-human CG-alpha(1-92)(N530, CR80)) is a specific example of a single chain gonadotropin having a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a CG alpha-subunit at the C-terminus, joined by a linker of 1-16 amino acids. The analogue la was derived from analogue 1 by removing the two glycosylation sites from the alpha-subunit. The analogue has anti-luteinising hormone (lutropin) activity and can be used for anti-luteinising hormone (lutropin) activity and reducing androgen secretion. The present sequence codes for analogue 1 a.

Sequence 836 BP; 166 A; 282 C; 222 G; 166 T;
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# ALIGNMENTS

Parsons, J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. TITLE The WashU-Merck EST Project JOURNAL Unpublished (1995)	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 601)  AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kuçaba, T., Le, M., Lennon, G., Marra, M.,	polylinker host-pHIDB (ampicillin resistant) Resitel-Wot I Resite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCGGATTTTTTTTTT	DEFINITION yw91b05.s1 Homo sapiens cDNA clone 259569 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.  ACCESSION N37759 NID 91153158 EST.  SOURCE human clone=259569 primer=m13 -40 forward library=Soares placenta	RESULT 1 LOCUS N32759 601 bp mRNA EST
ing,T., Soares,M., T Williamson,A., Wohld	ebrata; Gnathostoma apoda; Amniota; Mam Catarrhini; Homini ; Catiston, K., H a, T., Le, M., Lennon,	yrisu (Pharmacia) w one from 8 weeks an crand cDNA was prime sccGcGATTTTTTTTTTT s selected, ligated of I and cloned into vector (Pharmacia). and M. Fatima Bonald	clone 259569 3' sim PRECURSOR (HUMAN);	EST
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
1. .601
                                                                          Homo sapiens
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                                                                                                                                                                      GGACCAGCACCAGCTGTGGTGCC
                                                                                                                                                                                                    GGCNAAGCGGCTCCTTGGATGCC 457
                                                                                                                                                                                                                               CC-TGCAGCACGCGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTG
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yw95d03.s1 Homo sapiens cDNA clone 259973 3' similar CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);. 332604 g1153003 EST. human clone=259973 primer=m13 -40 forward library=Soa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Source: IMAGE Consortium, LINL
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
Location/Qualifiers
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Tel: 314 286 1800
Fax: 314 286 1810
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WashU-Merck EST Project
Washington University So
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                                                                                                            N32604
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High quality sequence stops:
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Similarity 96.2%;
426; Conservative
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/clone="257479"
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Pred. No. 0.00e+00;
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BASE COUNT
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JOURNAL
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Best Local Similarity
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TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGGCGCACCGTG
                                                                                                                                                                          GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCCC 315
                                                                                                                                                                                                                                                                               GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGGCAGCCAAGGGAAGCCGGAT 255
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                                                                                                         CTTGCAGCACGCGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGA 374
                                                                                                                                                    GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC
                                                                                                                                                                                                                                       GAGAGCCACGGCGTAGGAGACCACGGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Archonta; Primates; Catarrhini;

(bases 1 to 564)

Hillier, Clark, N., Dubuque, T., Ellistor
Holman, M., Hultman, M., Kucaba, T., Le, M., I
Parsons, J., Rifkin, L., Rohlfing, T., Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stops: 364
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trevaskis, E., Waterston, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polylinker host-DH10B (ampicillin resistant) Rsitel-Not I
Rsite2-Eco RI two placentae: one from 8 weeks and another from
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/clone="259973"
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Pred. No. 0.00e+00;
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son,A., Wohldmann,P. and
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Best Local Similarity
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                  GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT
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g1148556
EST.
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Sarcopterygil: Choanata; Tetrapoda; Amniotta; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Ht
1 (bases 1 to 548)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins,
Holman, M., Kucaba, T., Le, M., Lennon, G., Maa,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University Scho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-Merck EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trevaskis, E., Waterston, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human clone=258525 primer=m13 -40 forward library=Soares 8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a mod
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                                                                                                                                                                                          Conservative
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/clone="258525"
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                                                                                                                                                                                      Score 385; DB 13;
Pred. No. 0.00e+00;
0; Mismatches 6
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                                                                                                                                                                                                                                                                             206
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son,A., Wohldmann,P. and
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Length 593; Indels 4;

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JOURNAL COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
                                                                                                                                                                                                                                                                                                             Wilson, R.
The WashU-Merck EST
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                               Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 593)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yw78h03.s1 Homo sapiens cDNA clone 258389 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
                                                                                                 High quality sequence stops: 368
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human clone=258389 primer=ml3 -40 forward library=Soares placenta 8to9weeks 2NbHP8tc9W vector=p7713D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) Rsite1-Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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     109
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/clone="258389"
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                     Wilson, R.
The WashU-Merck EST
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11 (bases 1 to 442)
12 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yw81f08.sl Homo sapiens cDNA clone 258663 3' similar to CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
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95.3%;
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Pred. No. 0.00e+00;
0; Mismatches 17;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 364
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                        402;
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library
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CHORIOGONADOTROPIN BETA
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Similarity 94.6%;
402; Conservative
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/clone="258663"
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Fax: 314 286 1810
Email: escewatson.wustl.edu
High quality sequence stops: 225
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
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/clone="257711"
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               TGGACTCGAAGCGCAAATCGCGGGTAGTTGCACACCACCTGAGGCAGGGCGGCCAGACCC
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WashU-Merck EST Project
Washington University School of Medicine
14444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
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1 (bases 1 to 566)

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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                     human clone=259380 primer=ml3 -40 forward library=Soares placenta 8to9weeks 2NbHP8tc9W vector=PT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I -
                                                                                                                                                                                                       High quality sequence stops: 335
Source: IMAGE Consortium, LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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                    Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Lov
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 333
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human clone=258295 primer=m13 -40 forward library=Soares placenta 8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I -
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Hillier, L., Clark, N., Dubugue, T., Elliston, K., Hawkins, Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mar Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P., Wilson, R.
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Source: IMAGE Consortium, LLNL This clone is available royalty-free
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 640 Std Error: 0.00
                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
Tel: 314 286 1810
Fax: 314 286 1810
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Vertebrata;
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                                                                                                                                                                                                                                            GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCAC
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                                                                                                                                                                                                                                                                                    CTGCAGCACGCGGGTCATGGTGGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCTGCGGCGCAGAGTGCACATTGACAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGGGAGGGCCTTTGAGGAAGAGGAGGCCTGGAAGCGGGGGGTCATCACAGGTCAAGGG 139
                                                                                                                                                                                                                               GCACACGGGGCAGCCTCCTCTCCACAGCCAGGGTGGCATTGATGGGGGCGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGGGAGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG
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gli52015
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Luman clone=258890 primer=ml3 -40 forward library=Soares placenta buman clone=258890 vector=pp773D (Pharmacia) with a modified 8tc9weeks 2NDHP8tc9W vector=pp773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406;
                                                                                                                             yw84a02.sl Homo sapiens
CHORIOGONADOTROPIN BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the and Eco RI sites of the modified pTPT3 vector. Libr went through one round of normalization to Cot5, an constructed by Bento Soares and M. Fatima Bonaldo.
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/Organism "Homo sapiens"
/note "Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech was prepared from mRNA obtained from Clontech
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/db_xref="GDB:5924752"
120 c 190 g
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/clone="727841"
/clone_lib="Soares testis NHT"
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No. 0.00e+00;
                                                                                                                            clone 258890 3' similar
N PRECURSOR (HUMAN);.
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GGGGGGAGGGCCTTTNAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
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                      GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTTGATGGNGCGGCACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230
GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATT-GATGGGGCGGCACCGTG
                                                                                  CTGCAGCACGCGGGTCATGGTGGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT
                                                                                                           TTGCAGCACGCGGGTCATGGTGGGGGCAGTAACCGGCACAGATGGTGGTGTTGACGGTGAT
                                                                                                                                                                     GGACTCGAAGCGCACATCGCGGTAGTTGCACACCTGAGGCAGGGCCGGCAGGACCCC
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399; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stops: 329
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteic Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; The Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 446)
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/clone="258890"
<1. .>446
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Best Local Similarity 97.1%,
Matches 409; Conservative
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                                                                GTGGTCCTTGGGACCCCGACAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
                                                                                                                                            GGCAGGAGGGCCTTTAAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 135
                                      GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110
                                                                                                                      GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170
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g2569381
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4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          af62d08.s1 Soares NhIMPu S1 Homo sapiens cDNA clone 1046607 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
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1 (bases 1 to 526)
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/note="Organ: mixed (see below); Vector: pT773D-Pac
/note="Organ: mixed (see below); Vector: pT773D-Pac
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Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The dilver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 26032-265223,
340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Pooled
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/clone="1046607"
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Fax: 314 286 1810
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normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHHJW) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
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pregnant uterus"
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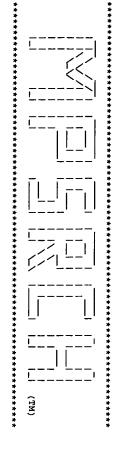
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                  Washington University School of Medicine 4444 Forest park Parkway, Box 8501, St. I Tel: 314 286 1810

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Unpublished (1995)
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T-CTCCACAGCCAGGGTGGCATTGAT-GGGGCGCACCGTGGACCAGC
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390; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares placenta 8to9weeks 2NbHP8to9w"
/dev_stage="two placentae: one from 8 weeks and an
from 9 weeks post conception"
/lab_host="DHIOB (ampicillin resistant)"
complement(<1. .>419)
a 109 c 168 g 63 t 6 others
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95.6%;
                                                                                                                                                                                                                                                                                                                                                     Score 351; DB 16;
Pred. No. 0.00e+00;
0; Mismatches 13
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Search completed: Wed May 6 15:04:47 1998 Job time : 1203 secs.

4)



Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Wed May 6 09:06:59 1998; MasPar time 10.23 Seconds 491.010 Million cell updates/sec

Title:

Description: Perfect Score Sequence: Score: >US-08-804-166-8 (1-336) from US08804166.pep 2541 1 SRTSLLLAFGLLCLPWLQEG..... SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 336

Searched: 120837 seqs, 14945562 residues Scoring table:

PAM 150 Gap 11

Post-processing: : Minimum Listing Match 0% first 45 summaries

Database:

a-geneseq31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part5 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 32.744; Variance 136.204; scale 0.240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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51.7	51.7	51.8	51.9	51.9	51.9	51.9	52.0	52.0		52.0	•			52.0	52.0	59.2	79.6	100.0	Query
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Mutant p55 tumour nec	Mutant p55 tumour nec	TNF-R-Pl. vivax Duffy	TNF-R-EBA 175 fusion	TNF-R-GBPH fusion pro	Human Tumour Necrosis	TNF-R-GBPH fusion pro	TNF-R-GBP 130 fusion	Human 55kD TNF-bindin	30kD TNF inhibitor pr	Lambda derived TNF-R.	TNF-alpha binding pro	p55 TNF-R.	TNF-alpha 55kD recept	TNF-R-GBP 130 fusion	Tumour Necrosis Facto	TBP(20-190)/hCG-alpha	TBP(20-161)/hCG-beta	TBP(20-190)/hCG-beta	Description
3.89e-119	3.89e-119	1.52e-119	9.50e-120	9.50e-120	9.50e-120	9.50e-120	5.93e-120	4.69e-120	4.69e-120	4.69e-120	4.69e-120	4.69e-120	4.69e-120	5.93e-120	4.69e-120	8.93e-139	7.11e-192	2.22e-245	Pred. No.

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61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120

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Query Match 100.0%; Best Local Similarity 100.0%; Matches 336; Conservative

Score 2541; DB 26; Pred. No. 2.22e-245; 0; Mismatches 0;

Length 336; Indels 0;

Gaps

0

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	
1013	1013	1013	1013	1014	1015	1015	1016	1018	1020	1020	1020	1021	1021	1021	1021	1022	1025	1030	1252	1263	1263	1291	1308	1313	1313	
39.9	39.9	39.9	39.9	39.9	39.9	39.9	40.0	40.1	40.1	40.1	40.1	40.2	40.2	40.2	40.2	40.2	40.3	40.5	49.3	49.7	49.7	50.8	51.5	51.7	51.7	
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Chorionic gonadotroph	Chorionic gonadotroph	hCG methionine substi	hCG/blH chimera, D7.	Chorionic gonadotroph	hCG histidine substit	Chorionic gonadotroph	Human CG beta-subunit	hCG histidine substit	hCG methionine substi		Human chorionic gonad	_	Single chain gonadotr	hCG/hLH chimera, A5.			Human chorionic gonad	н	TNF-alpha 5		kD TNF inhi	161)/hCG-alpha	receptor.	tant p55 tumour nec	p55 Tumour necrosis f	
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N-ESDB; 794008.

PF Hybrid dimeric protein comprising two co-expressed units - each per hybrid dimeric protein comprising subunit of a heterodimeric hased on receptor or ligand and a subunit of a heterodimeric per hormone, especially FSH, for inducing follicular maturation serious protein comprises 2 dimer forming co-expressed amino a rample; Pages 34-35; 60pp; English.

A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric creceptor chain or ligand, with ligand-receptor binding activity, bound directly or via a peptide linker to a subunit of a cheterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the the hormone's other subunits. The fusion protein, e.g. the check of the hormone's other subunits. The fusion protein, e.g. the chomopopeietin (TPO)/human chorionic gonadotrophin beta subunit (hGG-beta) fusion protein denoted by the present sequence, component, reducing the requirement for hormone itself and the cumber of injections needed.

So Sequence 307 AA;
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Matches 30
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20-FEB-1997; UO2315.

20-FEB-1996; US-011936.

(ISTF ) ARS APPLIED RES SI

Campbell RK, Chappel SC, Campbel RK, Chappel RK, 
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C. A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric creceptor chain or ligand, with ligand-receptor binding activity, bound directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit (hCG-alpha) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone
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Best Local S
Matches 19
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N-PSDB; T94021.
Hybrid dimeric protein com
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W33359;
19-MAR-1998
Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA. Tumour necrosis factor binding protein; TNF-BP; TNF-receptc pTNF-BP15; infectious disease; parasitic disease; cachexia; autoimmune disease; shock.
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R07449;
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20-FEB-1997; U02315.
20-FEB-1996; US-0119
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196; Conser
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Best Local Similarity 100.0%;
Matches 171; Conservative
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24-OCT 1990.
06-APR-1990: 106624.
21-APR-1989: DE-913101.
21-JUN-1989: DE-920282.
                            a receptor peptide.

Example A; Page 53-54; 93pp; English.

Hybrid peptides for binding cytokines, comprising a malaria parasite (plasmodium falciparum) peptide (capable of binding to a red blood cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples of these hybrid peptides. R70107 is a fusion of tumour necrosis factor receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) and glycophorin binding protein (GBP) 130. The use of cytokine can bind harmlessly to the RBC without deleterious effect. The RBC protects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanisms to TNF action Disclosure; Fig 1(1-3); Slpp; German.

Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of e.g. COS7 cells. The expressed proteins are useful prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or -beta (e.g. infectious parasitic diseases, shock, cachexia, autoimune diseases, adult respiratory distress syndrome etc., or side effects of treatment wit TNG-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R70107
R70107
                                                                                                                                                                                                 New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell
                                                                                                                                                                                                                                    Prendergast KF;
WPI; 95-115452/15.
                                                                                                                                                                                                                                                                   01-SEP-1994; G01900.
03-SEP-1993; GB-018350.
23-AUG-1994; GB-017021.
(PREN/) PRENDERGAST K F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KONTYCTCHAGFFLRENECYSCSNCKKSLECTKLCLPQIENVKGTEDSGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                                                                                                                                                                                                                                                                                                                                                                                                       peptide; malaria parasite; Plasmodium falciparum; fusion pro
ood cell; cytokine receptor; glycophorin binding peptide 130;
0; GBPH; glycophorin binding peptide homologue; glycophorin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q06282-Q06285.
371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                      falciparum
               excretion from the kidney, and due to steric
                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
 cytokines
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Pred.
0; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e 1322; DB 2;
. No. 4.69e-120;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I, Stratowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                 WO9207076-A.
30-APR-1992.
18-OCT-1991;
18-OCT-1990;
and probably represent a signal sequence. Residues 35-40 are highly charged (DREKR) and this is not normally found in secretory signal sequences. It is possible the receptor is processed by proteolysis after residue 40 which contains a dibasic cleavage site (RR). Hydropathy analysis of this sequence predicts a single transmembrane domain of 23 amino acids, dividing the sequence into an extracellular domain of 171 residues and a cytoplasmic domain of 221 residues. The sequence contains a large number of cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptid used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major merozoite surface antigen) and the Duffy binding receptor molecule (eg. exhibited by Plasmodium vivax). These peptides bind to pref. glycophorin A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid peptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological
                                                                                                                   treating autoimmune disease, septic shock, HIV etc.

Example; Fig 1; 43pp; English.

This sequence was deduced from human TNF-alpha cDNA isolated as in Q24440. The first 35 amino acids are generally quite hydrophobic Q24440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour necrosis factor alpha; extracellular binding domain; treatment; pulmonary diseases; septic shock; HIV infection; malaria; viral meningits; graft versus host disease;
                                                                                                                                                                                                                                   18-OCT-1990; GB-022648.
(CHAR-) CHARING CROSS S
Brennan FM, Feldmann M,
WPI; 92-167156/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNF-alpha 55kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R24000;
05-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                  New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for
                                                                                                                                                                                                                     N-PSDB; Q24440
                                                                                                                                                                                                                                                                                                                                                                                                            modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R24000 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KONTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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171; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                   G01826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor.
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential" " 151..153
                                                                                                                                                                                                                                                                                                                                                                                                                                                           145..147
                                                                                                                                                                                                                                                                                                                                                                             /label- N linked glycosylation site
/note- "potential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "potential"
[145.147]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 455
                                                                                                                                                                                                                                                                                                                                                /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label- signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%;
99.4%;
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                                                                                                                                                                                                                                                  SUNLEY
M, Gray
                                                                                                                                                                                                                                                                                                                                                transmembrane domain
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Pred.
0; M
                                                                                                                                                                                                                                                  PW,
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d. No. 5.93e-120;
Mismatches 1;
                                                                                                                                                                                                                                                  CENT.
Turner MJC;
                                                                                                                                                                                                                                                                                                                                                                                                                                           site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451;
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                                                                                                           are highly
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Best Local S
Matches 17
                                                                                                                                                         04-MAY-1995.
11-0CT-1994; 075742.
12-0CT-1993; IL-107268.
(YEDA) YEDA RES & DEV CO LTD.
Batkin M. Brakebusch C. Varfolomeev
This sequence represents human p55 tumour necrosis factor (TNF-R). Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell type. The only region of the receptor whose structure affects the shedding response is the spacer region (see R75012) in the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p55; tumour necrosis factor receptor; TNI
epidermal growth factor receptor; EGF-R;
phorbol myristate acetate; PMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residues, the arrangement of which is similar to that of other cell surface proteins, suggesting the TNF-alpha receptor is structurally related to a family of receptors.

NOTE: Residues 371,2 given in the sequence as T.L. are encoded by TGG (W) and AAG (K).

TGG (W) and AAG (K).
                                                                                 (TNF) receptor - from cell-bound TNF- r antagonising deleterious effects of TNF. Disclosure; Fig 1; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R75084 standard;
R75084;
                                                                                                            New protease capable of cleaving
                                                                                                                                      N-PSDB; Q90513
                                                                                                                                                                                                                                                         region
                                                                                                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                   misc_difference
                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kqntvctchagfflrenecvscsnckkslectklclpq1envkgtedsgtt 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KONTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 52.0%;
1 Similarity 100.0%;
171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                          /note= "major C terminus 202
                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                             /note=
198..2:
                                                                                                                                                                                                                                                                                                                                                                                                                /note- "glycosylation 161..163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note⊷ "N terminus of 54..56
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "glycosylation 145..147
                                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                                      /note= "minor C
212..234
                                                                                                                                                                                                                                                                                         /note= "essential for shedding reaction"
                                                                                                                                                                                                                                                                                                                                                                                                   'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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                                                                                                                                                                                                                                                                                                                                                              . 210
                                                                                                                                                                                                                                          "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                         "peptide used
                                                                                                                                                                                                                                                                                                                                               "spacer region"
                                                                                                                                                                                                                                                                                                                                                                                                  "glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1322; DB 4;
Pred. No. 4.69e-120;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                    terminus
                                                                                                        soluble tumour necrosis factor d TNF- receptor, useful for
                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                   site"
                                                                                                                                                                                                                                                                                                                                                                                                                           site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNF-R; human; murine; c
-R; protease; inhibitor;
                                                                                                                                                             Ħ
                                                                                                                                                                                                                                                                                                                                                                         creation
                                                                                                                                                                                                                                                                    for soluble
                                                                                                                                                                                                                                                                                                                    for soluble
                                                                                                                                                              Wallach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF-R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc domain. This region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane domain. The cc spacer region of the encoded protein was used to create the chimeras between human p55 TNF-R and murine epidermal growth factor receptor (EGF-R) that are represented by R75007-11. This spacer region was cc subjected to deletion mutations (R75013-25) and substitutions (R75013-25) and substitutions was cc (R75026-47). Of the spacer region, the most important residues are cc Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most comportant of these. The shedding of the receptor is independent of the conformation of these residues, with the exception of a limited component of the protein adversely effect the shedding process. Cc conformation of the protein adversely effect the shedding process. Cc The mutations shown in R75013-47 were introduced in order to create an cc inhibitor of a protease that is capable of cleaving the soluble TNF-R cc from the cell bound TNF-R. Fragments of these inhibitors can be seen in cc used for enhancing TNF function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                             05-FEB-1992.
05-FEB-1992.
15-JUN-1990; GB-013410.
15-JUN-1990; GB-013410.
(CHAR-) CHARING CROSS SUNLE
Feldman M, Gray P, Turner M
WPI; 92-043613/06.
N-PSDB; Q20973.
useful in treating the cytokine.

e.g. rheumatoid arthritis
Disclosure; Fig 1; 25pp; English.
The amino acid sequence is that of tumour necrosis factor alpha binding protein which contains the extracellular domain of human binding protein. It is soluble and can be used in the regulation of alpha receptor. It is soluble and sequestering the cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R20787
                                                                                                                                                                                                                                                                            GB2246569-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis extracellular d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF-alpha binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R20787;
11-MAY-1992
                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                               ew tumour necrosis factor alpha binding protein and polypeptide useful in treating cachexia, sepsis and auto immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
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1 Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                         "potential N-glycosylation
                                                                                                                                                                                                                                                                                                                                                          "transmembrane domain"
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Pred. No. 4.69e-120;
0; Mismatches 0;
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Best Local
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                                                                           The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. disclosure; Page 57-59; 85pp; English.

The sequences given in R42058-59 repressent human tumour necrosis factor receptor (TNF-R) and the sequences in R42060-61 represent human interleukin-1 receptor (IL-IR). These sequences were used the production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-1R; fusion protein; linker; TNF; IL-1, cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft verses host disease; sepsis; inflammation; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R42059
R42059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1993; U02938.
30-MAR-1992; US-860710.
(IMMV) IMMUNEX CORP.
  host disease, sepsis, so autoimmune dysfunctions Sequence 455 AA;
                                                                                                                                                                                                                                                                                                                                                                                          TNF-R-linker-TNF-R-linker-IL-1R
IL-1R-linker-TNF-R-linker-TNF-R
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N-PSDB; Q49932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-1994
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Pred. No. 4.69e-120;
0; Mismatches 0;
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Best Local :
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18-JUL-1989; US-381080.

11-DEC-1989; US-450329.

07-FEB-1990; US-479661.

(SYNE-) SYNERGEN INC.

WPI; 91-073847/11.
                                    JLT 11
R11082 standard; Prof
R11082;
24-MAY-1991 (first 6
                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor inhibitor - for suppression of TNF-alph and -beta, useful as therapeutic agent.

Disclosure; Fig 21; 142pp; English.

The sequence comprises the entire 30 kD TNF inhibitor. The clo from which the sequence was deduced was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA. library prepd. from second into expression vectors for pre of TNF inhibitor for use in the treatment of inflammatory and degenerative diseases. The active protein is claimed (Claim 8 degenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 10
R10986
R10986
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                                                                                                                                                                                                                                                                                                                                       degenerative diseases. The 
See also R10984 and R11001.
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Local Similarity 100.0%;
hes 171; Conservative
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1 Similarity 100.0%;
171; Conservation
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Pred. No. 4.69e-120;
0; Mismatches 0;
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Pred. No. 4.69e-120;
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24-MAY-1991 (110)
Human 55kD TNF-binding protein.
Tumour Necrosis Factor; binding proteins; septic shock;
Tumour Necrosis Factor; lymphokine; cytokine.

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PRR COSS COST HEROTE
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                                                                                                                      R70103 standard; Protein; 90 R70103; 02-NOV-1995 (first entry) TNF-R-GBP 130 fusion protein Hybrid peptide; malaria para red blood cell; cytokine rec GBP 130; GBPH; 91ycophorin l Chimeric Homo sapiens. Chimeric Plasmodium falcipal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP-417563-A.
20-MAR-1991.
31-AUG-1990; 116707.
12-SEP-1989; CH-003319.
08-MAR-1990; CH-000746.
20-APR-1990; CH-001347.
                    W09506737-A.
09-MAR-1995.
01-SEP-1994;
03-SEP-1993;
23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial amino acid sequences were determined for the 55 and 75kD TNF-BPS (see Ri1072-Ri1081) and oligonucleotide primers were synthesised based on these partial sequences. The primers were used to produce a cDNA fragment for use as aprobe to screen a human placental cDNA bank constructed in lambda gtll. Positive clones were identified and sequenced. DNA constructs comprising the TNF-BP coding sequence may also contain a fragment encoding a human Ig domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   improved TNF-binding properties.
See also Q10956.
Sequence 455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insoluble tumour necrosis factor binding encoding them, useful in pharmaceutical particular in the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOFF ) HOFFMANN-LA
Brockhaus M, Dembic
Schlaeger EJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
                                                                                                                                                                                                                                                                                                                                                                                                         KONTYCTCHAGFFLRENECYSCSNCKKSLECTKLCLPQIENYKGTEDSGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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                                                                                                                                                                       peptide; malaria parasite; Plasmodium falciparum; fusion protein; cod cell; cytokine receptor; glycophorin binding peptide 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 52.0%;
l Similarity 100.0%;
171; Conservative
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; G01900.
; GB-018350.
; GB-017021.
NDERGAST K F.
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270
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151
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212..230
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Z, Gen
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                                                                                                                                                                                                                                                                                                                   900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1322; DB 2; | Pred. No. 4.69e-120; | 0; Mismatches 0;
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    and DNA
for antil

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IRESULT
ACCOMENTATION
ACCOMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pri malaria parasite peptide capable of binding a red blood cell and prepride.

Example A: Page 46-47; 93pp; English.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite CC (Plasmodium falciparum) peptide (capable of binding to a red blood CC (Plasmodium falciparum) peptide are claimed. R70103-25 are examples CC (Plasmodium falciparum) peptide are claimed. R70103-25 are examples CC ell (RBC)) and a receptor peptide are claimed. R70103-25 are examples CC of these hybrid peptides. R70103 is a fusion of tumour necrosis factor CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) CC and glycophorin binding protein (GBP) 130. The use of cytokine can bind CC thindrance prevents the cytokines means that the cytokine can bind CC hybrid peptides from excretion from the kidney, and due to steric CC hindrance prevents the cytokines binding to a receptor in another cell. CC GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides used, others include EBA 175 (175 kDa erythrocyte binding antigen), CC PMMSA (pre major merozoite surface antigen) and the Duffy binding CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on CC the surface of RBCs. The hybrid peptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                              WO9506737-A.
09-MAR-1995.
01-SEP-1994; G01900.
03-SEP-1994; GB-018350.
23-AUG-1994; GB-017021.
(PREN/) PRENDERGAST K F.
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WPI; 95-115452/15.
New hybrid peptide(s) i
malaria parasite peptik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion red blood cell; cytokine receptor; glycophorin binding peptide GBP 130; GBPH; glycophorin binding peptide homologue; glycophor tumour necrosis factor receptor; TNF-R. Chimeric Homo sapiens.
a receptor peptide.
Example A; Page 54-55; 93pp;
Hybrid peptides for binding c
(Plasmodium falciparum) pepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 13
R70108 standard; Protein;
R70108;
10-NOV-1995 (first entry)
                                                                                                                                                 Prendergast KF;
WPI; 95-115452/15.
New hybrid peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    key Location/Qualifiers misc_difference 230..269
                                                                                                             New hybrid peptide(s) for binding cytokine(s) malaria parasite peptide capable of binding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF-R-GBPH fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kqntvctchagfflrenecvscsnckkslectklclpqlenvkgtedsgtna 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 52.0%;
l Similarity 99.4%;
171; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             number"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= repeat_region
/note= "can be repeated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
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  93pp; English.
ding cytokines, comprising a
peptide (capable of binding
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Pred. No. 5.93e-120;
0; Mismatches 1;
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of binding a
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                                                                                                                   comprising a blood cell
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ed blood cell and
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  malaria parasite
to a red blood
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                                                                                                                   and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples CC of these hybrid peptides. R70108 is a fusion of tumour necrosis factor CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) CC and 91ycophorin binding protein (GBP) homologue (GBPH). The CC use of cytokine receptors not normally found on RBCs means that the CC cytokine can bind harmlessly to the RBC without deleterious effect. CC The RBC protects the hybrid peptides from excretion from the kidney, and CC due to steric hindrance prevents the cytokines binding to a receptor in CC another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides CC used, others include EBA 175 (175 kDa erythrocyte binding receptor CC composed to the surface antigen) and the Duffy binding receptor CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to CC pref. 91ycophorin A, B and C, stalo 91ycoproteins, found on the surface CC cytokines in the circulation to reduce pathological damage.
    веst Local
Matches 1
                                                                                                        The encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanismsm to TNF action Disclosure; Fig 91(1-2); 51pp; German.

S Disclosure; Fig 91(1-2); 51pp; German.

C LambdarNF-R2 encodes the complete human TNF-R2 and was used to screen the HS913T cDNA library.

C LambdarNF-R2 encodes the complete human TNF-R2 and was used to construct a plasmid (pADTNF-R) expressing the product the same way as pADTNF-BP (see Q06282). The expressed proteins are useful prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock, cachexia, autoimmune diseases, adult respiratory distress syndrome etc., or side effects of treatment with assaying TNF and in study of TNF-receptor interactions.

C See also Q06282-Q06285.
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                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-1990; 106624.
21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT.
Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa WPI; 90-321987/43.
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Example A; Page 47-48; 93pp; English.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite (Plasmodium falciparum) peptide (capable of binding to a red blood CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples of these hybrid peptides. R70104 is a fusion of tumour necrosis factor creceptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359) CC and glycophorin binding protein (GBP) homologue (GBPH). The use of CC cytokine receptors not normally found on RBCs means that the Cytokine receptors not normally found on RBCs means that the Cytokine can bind harmlessly to the RBC without deleterious effect. CC The RBC protects the hybrid peptides from excretion from the kidney, and CC due to steric hindrance prevents the cytokines binding to a receptor in CC another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major merozoite surface antigen) and the Duffy binding receptor conlecule (eg. exhibited by Plasmodium vivax). These peptides bind to CC pref. glycophorin A, B and C, sialo glycoproteins, found on the surface cytokines in the circulation to reduce pathological damage.

Se Sequence 547 AA;
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03-SEP-1993;
23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hybrid peptide(s) for binding malaria parasite peptide capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cytokine receptor; glycophorin binding peptide 130; GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A; tumour necrosis factor receptor; TNF-R.
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WPI; 95-115452/15.
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23-AUG-1994; GB-017021.
(PREN/) PRENDERGAST K F.
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09-MAR-1995.
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Chimeric Plasmodium fa
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R70104 standard;
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed May 6 09:05:45 1998; MasPar time 14.61 Seconds 839.893 Million cell updates/sec

Title: >US-08-804-166-8 (1-336) from US08804166.pep 2541

Description: Perfect Score: Sequence: 1 SRTSLLLAFGLLCLPWLQEG......PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150 Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 42.414; Variance 82.038; scale 0.517

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score
No.	1322
1	1257
2	1238
3	1121
40078	1121 1105 1030 1030
10 9 6	1028
12	960
12	960
13	944
14	857
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13.9	14.2	14.4	14.5	15.3	15.7	15.9	15.9	16.0	16.2	16.4	16.5	16.8	16.8	16.9	22.9	23.0	23.1	23.4	23.4	23.5	
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luteinizing hormone b	gonadotropin II beta	luteinizing hormone b	lutropin beta chain p	n II beta	beta cha	gonadotropin II beta	lutropin beta chain -	gonadotropin beta cha	gonadotropin II beta	II beta	gonadotropin II beta	beta cha	gonadotropin beta cha	gonadotropin beta cha	luteinizing hormone b	lutropin beta chain -	lutropin beta chain p	lutropin beta chain p	lutropin beta chain -	lutropin beta chain p	TOTAL PROPERTY OF
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# ALIGNMENTS

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H.; Kohr, W.J.; Goeddel, D.V. Cell (1990) 61:361-370 Molecular cloning and expression of a tumor necrosis factor. nces MUID:90235285 A34900 Ltype mRNA L-455 ##label SCH 1-455 ##label SCH ferences GB:M33294; NID:g339744; PID:g3:	5 HA I	A34899  A34899  authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, W.  yournal Cell (1990) 61:351-359  title Molecular cloning and expression of the human 55 kd tumor  necrosis factor receptor.  cross-references M010:90235284	Ha I'	tumor necrosis factor receptor type 1 precursor - humanALTERNATE_NAM tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein 1 (TNF blocking factor) #formal_name Homo sapiens #common_name man 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 24-Oct-1997 #38208; A34999; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38258; A60594; A35010; JC2404 A38208	GQHUT1 #type complete

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                                                                                                                                                                           #journal Eur. J. Immunol. (1990) 20:1167-1174

#title Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.

#cross-references MUID:90292116

#accession A60231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, H.; Wallach, D.
#journal EMBO J. (1990) 9:3269-3278
#title Soluble forms of tumor necrosis factor receptors (TNF-Rs).
The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384

*title Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protein

#cross-references MUID:91017509

#accession A38281
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##residues 30.38;41.53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
##residues 107-128;162-167,'X',169-201 ##label HI2
the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
                                                                                                                  ##molecule_type protein
#residues 41-43,'X',45-53,'X',55-57 ##label SEC
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##cross-references EMBL:X55313; NID:g37223; PID:g37224
##note parts of soluble TNF binding protein 1, including its
#mino and carboxyl ends, were confirmed by protein
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##cross-references GB.M37764
##note the authors translated the codon TGG for residue 371
##note Thr, AAG for residue 372 as Leu, and GAC for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                     **molecule_type DNA
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A38258
Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; R.S.; Granger, G.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene (1993) 134:209-216
Cloning and partial characterization of the promoter human p55 tumor necrosis factor (TNF) receptor.
JT0758
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DNA Cell Biol. (1990) 9:705-715
Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
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Gene (1993) 134:209-
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  Query Match 52.0%;
Best Local Similarity 100.0%;
Matches 171; Conservative
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168-196
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*cross-references MUID:91062364
*accession A38258
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##residues 41-53,'x',55-144,'x',146-150,'x',152-186,'x',188-201
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##residues 41-43,'X',45-53,'Y',55-57,'XK',60 ##label
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. (1990) 265:1531-1536
Two tumor necrosis factor-binding proteins purified from
human urine. Evidence for immunological cross-reactivity
with cell surface tumor necrosis factor receptors.
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*product TNF binding protein 1 (tumor necrosis factor
alpha inhibitor) *status experimental *label TBP1\
*domain NGF receptor repeat homology *label NG2\
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*domain NGF receptor repeat homology *label NG4\
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predicted #label MAT\
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Score 1322; DB 1; I
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Resolution: 1.85 angstroms
Determination: X-ray diffrac
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binding
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H.J.; Broger, C.; Loetscher, H.; Lesslauer, W
Cell (1993) 73:431-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor necrosis factor receptor extracellular domain, chain pertracellular domain of the 55kda tumor necrosis factor receptor. crystallized at ph3.7 in p 21 21 21. #formal_name Homo sapiens #common_name man expressed in Escherichia coli, the construct contains residues 12 to 172 of the mature sequence of the entire receptor. residue 11 is mutated to met as a result of the
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Crystallographic evidence for dimerization of unliganded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications f
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J. Mol. Biol. (1994) 239:332
Two crystal forms of the extracellular domain of
                  #length
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Best Local Similarity 100.0%;
66-86
88-104
107-119
110-127
129-140
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73-76,85-87
92-98,101-106
113-117,126-129
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                                                                                                                                                                                                                                                                                                             Resolution: 1.85 angstroms
Determination: X-ray diffraction
R-value: no refinement
binding protein; cytokine;
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H.J.; Broger, C.; Lo
Cell (1993) 73:431-445
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Crystallographic evidence for dimerization of unliganded tumor necrosis factor receptor.
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extracellular domain of the 55kda tumor necrosis factor
receptor. crystallized at ph3.7 in p 21 21 21.
#formal_name Homo sapiens #common_name man
expressed in Escherichia coll, the construct contains
residues 12 to 172 of the mature sequence of the entire
receptor, residue 11 is mutated to met as a result of the
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Two crystal forms of the extracellular
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Pred. No. 1.30e-238;
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cher, H.; Lesslauer,
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COMMENT
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DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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Resolution: 2.25 angstroms
Determination: X-ray diffraction
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Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for
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Two crystal forms of the extracellular domain of
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H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
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Pred. No. 4.07e-209;
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Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gent
Lesslauer, W.
J. Mol. Biol. (1993) 229:555
Crystallization and preliminary analysis of tnf-bet.
tnf-beta-55 kd tnf receptor complex.
Resolution: 2.85 angstroms
Determination: X.ray diffraction.
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Similarity 100.0%;
139; Conservative
tumor necrosis factor receptor 55 kd extracellular domain contains residues 12 172 of the mature receptor sequence, chain A - hu stnfr1; type i receptor
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Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for receptor activation.
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H.J.; Broger, C.; Loetscher, H.; Lesslauer, W
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Pred. No. 1.18e-205;
0; Mismatches 0;
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                                                                                                                                                #authors Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature (1984) 307:37-40

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                       ##residues 1-145 ##label RES ##cross-references EMBL:X00265; NID:g31719
                                                 ##molecule_type DNA
##residues 1-1
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Two crystal forms of the extracellular domain
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expressed in Escherichia coli, residue
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Pred. No. 3.86e-204;
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Best Local :
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                                                                                                                                   #authors Policastro, P.F.; Daniels-McQueen, S.; Carle, #journal J. Biol. Chem. (1986) 261:5907-5916 #title A map of the hCG beta-LH beta gene cluster. #cross-references MUID:86195987 #accession I55250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Fiddes, J.C.; Goodman, H.M.
#journal Nature (1980) 286:684-684
#title The cDNA for the beta-subunit of human chorionic gonadotropin
suggests evolution of a gene by readthrough into the
3'-untranslated region.
#cross-references MUID:81012134
#accession A93230
#accession
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##cross-references GB:J00117; GB:M38559; GB:M54963; NID:g180436;
PID:g180437
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                       ##note
                                                                      ##molecule_type DNA
##residues 1-5 ##label PO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1-165 ##label POL
##cross-references GB:K03189; NID:g180450; PID:g180453
##note clone CG-beta-e
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                                               ##cross-references GB:M13504;
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139; Conservation
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J. Biol. Chem. (1983) 258:11492-11499

The beta subunit of human chorionic gonadotropin is encoded
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                                            NID:g180419; PID:g463088
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fauthors Morgan, F.J.; Birken, S.; Canfield, R.E.

#Journal J. Biol. Chem. (1975) 250:5247-5258

The amino acid sequence of human chorionic

#title The amino acid sequence of human chorionic

#title alpha subunit and beta subunit.

#cross-references MUID:75211304
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#title
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**BIRKen, S.; Fetherston, J.; Canfield, R.; Boime, I.

**Journal J. Biol. Chem. (1981) 256:1816-1823

The amino acid sequences of the prepeptides contained **title alpha and beta subunits of human choriogonadotropin.

**Ecross-references MUID:81117268
#cross-references MUID:93229246
#accession B56873
#accession B56873
#accession B56873
#amolecule_type protein
26-28'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X'
##residues 26-28'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X'
##residues 78-91,'G',93-102 ##label KAR
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*authors Carlsen, R.B.; Bahl, O.P.; Swaminathan,
*journal J. Biol. Chem. (1973) 248:6810-6827
*cross-references MUID:74011267
*accession A92142
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##residues 21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP'
##residues ##label CAR
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**molecule_type DNA
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Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.;
Agosto, G.M.; Krichevsky, A.; Vaitukaitis, J.L.; Canf
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The immunological characteristics of the enzymatic fragments of human chorionic gonadotropin beta-subunit.
                                                                                                         A56873,

Kardana, A.; Bagshawe, K.D.; Coles, B.;

Br. J. Cancer (1993) 67:688-692

Characterisation of UGP and its relation
                                                                                                                                                                                                                                                                                                    Endocrinology (1988) 123:572-583
Structure of the human chorionic gonadotropin beta-subunit fragment from pregnancy urine.
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Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li,
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54-108,58-110,
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                                                                            ##residues 1-461 ##label
##cross-references GB:U19994;
               ##molecule_type protein
##rosidues 1-7 ##label SU2
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ip_position 19q13.3-19q13.3
##experimental_source kidney cell line
                                                                                                                           ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLPSPSRLPGPSDTPILPQ 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLPSPSRLPGPSDTPILPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.5%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Grants;
(or pseudogenes)
*superfamily pituitary glycoprotein
*superfamily hormone; pituitary
                                                                                                                                                    JC4302
                                                                                                                                                                                     Suter, B.; Pauli, U.
Gene (1995) 163:263-266
Cloning of the cDNA encoding
                                                                                                                                                                                                                                                                                                   tumor necrosis factor receptor p55 - pigORGANISM
29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
12-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted\
    *binding_site carbohydrate (Ser) (covalent) *status
    experimental
    *length 165    *molecular-weight 17739    *checksum 6523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature (1994) 369:455-461 crystal structure of human chorionic gonadotropin. annotation; X-ray crystallography, 3.0 angstroms; of disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.;
J.W.; Canfield, R.E.; Machin, K.J.; Morgan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the choriogonadotropin beta chain locus contains
                                                                                                                                                                                                                                                                               JC4302; PC4093
                                                                                                                                                                                                                                                                                                                                                                                           JC4302
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                                                                                                                                                                        factor receptor.
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this material was designated urinary
peptide (peak 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #disulfide_bonds #status experimental\
#binding_site_carbohydrate (Asn) (cova
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#product choriogonadotropin beta chain #status
experimental #label MAT\
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Pred. No. 1.88e-189;
0; Mismatches 0;
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NID:g1141752;
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                                                                                     PID: g1141753
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F.J.; Isaa
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Best Local S
Matches 13
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Best Local
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211-231
361-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
#Journal Nature (1984) 307:37-40
#title Evolution of the genes for the beta subunits of human chorionic gonadotropin and luteinizing hormone.
#cross-references MUID:84093590
#accession 137231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-29
30-461
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##resian--
                     127
                                                                                                                                                 198
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                                                                                                                                                                                                                                                 Match 40.3%;
Local Similarity 99.3%;
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                                                                                                                                                                  7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                           SLPSPSRLPGPSDTPILPQ 145
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                                                                                                       IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPPP 126
                                                                                                                                                 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%;
Similarity 73.1%;
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   receptor repeat homology
glycoprotein; kidney; receptor; transmembrane protein; tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tnfr
                                                                                                                                                                                                                                                                                                                 #superfamily pituitary glycoprotein hormone beta chain
#length 145 #checksum 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-gonadotropin - human (fragment)ORGANISM #fc
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
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#product tumor necrosis factor receptor p55 #status
predicted #label MAT\
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                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:X00266; NID:g29907
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transmembrane #status predicted #label T
                                                                                                                                                                                                                                                   Score 1024; DB 2;
Pred. No. 3.70e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1028; DB 2;
Pred. No. 5.08e-189;
24; Mismatches 21;
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                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
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                                                                                                                                                                                                                                                                       Length 145
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FEATURE
1-29
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REFERENCE
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                                         KEYWORDS
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                                                                                                                        COMMENT
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                                                                                                                                                                                                                                                                                                               #authors
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannar C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.

#journal Mol. Cell. Biol. (1991) 11:3020-3026

#title Molecular cloning and expression of the type 1 and type 2

murine receptors for tumor necrosis factor.

#cross-references MUID:91246168
                                                                                                                                                                                                                                                   #journal Immunogenetics (1994) 39:450-451
#title Nucleotide sequence of the TNF t
endotheliama cell line.
#cross-references MUID:94245292
                                                                                                                                                                                                                                                                                                                                                                                                                                              #cross-references MUID:92039815
#accession S19021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p55 tumor necrosis factor receptor.
#cross-references_MUID:91285014
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#accession A38634
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##cross references GB:M60468; NID:g199825; PID:g199826
ENCE S16677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318
                                                         ##residues 1-454 ##label RES
##cross-references GB:L26349; NID:9430732; PID:9430733
#This protein is one of two distantly related receptors
TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
FIFICATION #superfamily tumor necrosis factor receptor type
receptor repeat homology
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##residues 1-454 ##label ROT
##cross-references EMBL:X57796; NID:g54848; PID:g54849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-454 ##label BAR ##cross-references EMBL:X59238; NID:g53578; PID:g53579
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Molecular cloning and expression of the mouse Tnf re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
Eur. J. Immunol. (1991) 21:1649-1656
Cloning, expression and cross-linking analysis of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834 Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAM #formal_name Mus musculus #common_name house mouse 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Sep-1997
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                                         duplication;
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#domain signal sequence #status
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                                         glycoprotein; receptor; transmembrane protein
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54,151,202
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#journal Mol. Immunol. (1993) 30:165-176

#title Genomic organization and promoter function
tumor necrosis factor receptor beta gene.

#cross-references MID:93156721
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44-82
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                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **status preliminary; translated from GB/EMBL/DDBJ
*#molecule_type DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-454 ##label RES 1-454 ##label RES
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                                                                                                                                                                                                                                                                                                                                                                            41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 68.6%;
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Local Similarity 68.6%;
les 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                  TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TONTYCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
                                                                                                                                                                                                                                                    SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
                                                                                                                                                                                                                                                                                                                                      DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KONTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ-IENVKGTEDSGTT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
                                                KONTYCTCHAGFFLRENECYSCSNCKKSLECTKLCLPQ-IENVKGTEDSGTT 193
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                                                                                                                                                                                        SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokine receptor #length 454 #molecular-weight 50030 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; #superfamily tumor necrosis factor receptor type 1; No receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I57826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length
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#domain NGF receptor repeat homology *label NG3\
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Pred. No. 2.26e-174;
27; Mismatches 26; Indels
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Pred. No. 2.26e-174;
27; Mismatches 26;
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Best Local S
Matches 11
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Stratowa, C.; Adolf, G.R.

#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
#accession B36555
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84-126
127-167
168-204
212-234
235-461
54,151,201
   #authors
#journal
#title
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##cross-references GB:M63122; NID:g207361; PID:g207362

##cross-references GB:M63122; NID:g207361; PID:g207362

NT This protein is one of two known receptors for both TNF-alpha
(Cachectin) and TNF-beta (lymphotoxin).

(Cachectin) and TNF-beta (lymphotoxin)

(Cachectin) and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTA 211
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Local Similarity 67.3%;
es 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KONTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT
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   Crawford, R.J.; Tregear, Gene (1986) 46:161-169
The nucleotide sequences
                                                                                                                                                                                #common_name olive baboon
31-Mar-1988 #sequence_revision
03-May-1996
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                                                                           Crawford,
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#domain NGF receptor repeat homology *label NG2\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 944; DB 1; L. Pred. No. 6.21e-171; 25; Mismatches 31:
                                                                       G.W.; Niall,
of baboon chorionic
                                                                                                                                                                                                                      31-Mar-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 461;
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                                                                           H.D
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   gonadotropin
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RESULT

TITLE

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SUMMARY

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COMMENT
COMMENT
KEYWORDS
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REFERENCE
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1-20
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#authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.7%; Score 857; DB 1; Length 165; Best Local Similarity 81.3%; Pred. No. 2.82e-152; Matches 113; Conservative 14; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-77,43-92,46-130,
54-108,58-110,
113-120
33,50
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##molecule_type mRNA
1-16
                                                                                                                                                                                                                                            #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                             #journal #title
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                           97-101,26-39,9-17
54-59,86-91
61-67,78-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #submission submitted to
#cross-references PDB:1XUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140,147,152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVVCNYREVRFES 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLPSPSRLPGPSDTPILPQ 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sidues 1-165 ##label CRA
There are at least five copies of CG-related genes and at least two
of these are expressed in the baboon placenta.
TION #superfamily pituitary glycoprotein hormone beta chain
glycoprotein; hormone; placenta; pregnancy maintenance
                                                                                                                   Resolution: not applicable
Determination: theoretical model
complex; glycoprotein hormone
phosphorylation; receptor
                                                                                                                                                                                                                                                                                                                                                         Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythi
Wu, H.; Hendrickson, W.A.; El Tayar, N.
Structure (London) (1996) 3:1341
Structural predictions for the ligand-binding region
glycoprotein hormone receptors and the nature of
hormone-receptor interactions structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N. submitted to the Brookhaven Protein Data Bank, December 1996
                                                                                                                                                                                                       Hendrickson, W.A.

Structure (London) (1994) 2:545

Structure of human chorionic gonadotropin at 2.6 a from mad analysis of the selenomethionyl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chorionic gonadotropin, chain B - humanPDB_TITLE
   receptor complexed with human chorionic gonadotropin
   formal_name Homo sapiens #common_name man
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#length 165 #molecular-weight 17592 #checksum 4960
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#region beta sheet\
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#disulfide_bonds\
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#product choriogonadotropin beta chain #status predicted
#label CGB\
                                                                                                                                                                                                                                                                                                             Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
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                                                                                                                                            receptor glycoprotein; hormone,
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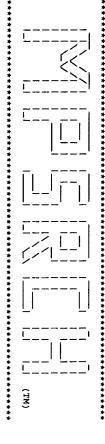
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                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                                                                               Query Match 31.6%;
Best Local Similarity 100.0%;
Matches 105; Conservative
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33-87
37-89
92-99
                                                258
                                                                                                                198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
                                                                   66 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 110
                                                                                                                                  6 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 65
                                                IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 302
                                                                                                                                                                                                                                                 #disulfide_bonds\
#disulfide_bonds\
#disulfide_bonds\
#disulfide_bonds
#disulfide_bonds
#length 110 #molecular-weight 11906 #checksum
6 09:06:41 1998
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Pred. No. 9.67e-141;
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Search completed: Wed May Job time : 56 secs.

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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein protein database search, using Smith-Waterman algorithm
Run on: Wed May 6 09:03:29 1998; MasPar time 9.80 Seconds
859.610 Million cell updates/sec

Title: >US-08-804-166-8

Description: (1-336) from US08804166.pep
Perfect Score: 2541

Sequence: 1 SRTSLLLAFGLLCLPWLQEG......PSLPSPSRLPGPSDTFILPQ 336

Tabular output not generated.

searched: 69112 seqs, 25083644 residues

Scoring table:

PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35

Statistics: Mean 44.259; Variance 72.852; scale 0.608

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Re

45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24
281	289	297	303	306	305	308	309	309	310	320	319	352	355	366	371	388	398	403	405	407	411
11.1	11.4	11.7		12.0		12.1	12.2							14.4	14.6		15.7	15.9	15.9	16.0	16.2
129	129	118	130	138	130	138	138	138	138	138	136	159	115	166	128	142	142	140	112	113	142
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FSHB_HUMAN	FSHB_SHEEP	FSHB_HORSE	FSHB_RAT	TSHB_MOUSE	FSHB_MOUSE	TSHB_HUMAN	TSHB_BOVIN	TSHB_RAT	TSHB_PIG	TSHB_CANFA	GTH2_FUNHE	LSHB_MELGA	GTH2_THUOB	LSHB_COTJA	LSHB_STRCA	GTH2_CORAU	GTHB_ONCTS	GTH2_ANGAN	LSHB_RANCA	GTHB_MURCI	GTHZ_UNCMA
FOLLITROPIN BETA	FOLLITROPIN BETA	FOLLITROPIN BETA	FOLLITROPIN BETA	THYROTROPIN BETA	FOLLITROPIN BETA	THYROTROPIN BETA	GONADOTROPIN BE	LUTROPIN BETA CHAIN	GONADOTROPIN BE	LUTROPIN BETA C	LUTROPIN BETA C	GONADOTROPIN BE	GONADOTROPIN BE	GONADOTROPIN BE	LUTROPIN BETA CHAIN	GONADOTROPIN BE	GUNADOTROPIN BE				
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1.30e-38	2.07e-40	3.24e-42	1.42e-43	2.95e-44	4.98e-44	1.03e-44	6.13e-45	6.13e-45	3.63e-45	1.89e-47	3.20e-47	7.92e-55	1.59e-55	4.38e-58	2.98e-59	3.09e-63	1.37e-65	9.05e-67	3.05e-67	1.03e-67	1.1be-b8

# ALIGNMENTS

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                                                                                                                 SEQUENCE FROM N.A.
TISSUE-PLACENTA;
MEDLINE; 91017509.
GRAY P.W., BARRETT K., (
PROC. NATL. ACAD. SCI. U
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MEDLINE; 90235284 Y.-C.E.,
LOSTISCHER H., PAN Y.-C.E.,
TABUCHI H., LESSLAUER W.;
CELL 61:351-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 4 MEDILINE; 91006021.

NOPHAR Y., KEMPER O., BRAKEBUSCH C., ADERKA D., HOLTMANN H., WALLACH D.; EMBO J. 9:3269-3278(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                            MEDÎLINE; 91090841.
HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
DNA CELL BIOL. 9:705-715(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 90235285.
SCHALL T.J., LEWIS M., KOLL
GETANAGA T., GRANGER G.A.,
CELL 61:361-370(1990).
   FUCHS P.,
                               SEQUENCE FROM N.A. MEDLINE; 92250049.
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TISSUE-PLACENTA;
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   DWORZAK M., HIMMLER A., AMBROS P.F.;
                                                                                                                        CHANTRY D., TURNER M., FELDMAN M.;
U.S.A. 87:7380-7384(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAHM H.-W., GENTZ R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGELMANN H.,
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DB; 1N-
PDB; 1EXT;
MIM; 191190;
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PROSITE; PS*
PROSITE; P
"CEPTOR"
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[7]
SEQUENCE OF 41-45.
MEDILINE: 90110215.
ENGELMANN H., NOVICE
                                                                                                                                                                                                                                                                                     RECEPTOR; TRA
3D-STRUCTURE.
SIGNAL
             TRANSMEM
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CHAIN
DOMAIN
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BANNER D.W., D'ARCY A., GROGER C., LOETSCHER H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS)
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1NCF; 07-DEC-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90110215.
N H., NOVICK D., WALLACH D.;
CHEM. 265:1531-1536(1990).
                                                                                                                                                                                                                                                                                                                                    PS00652; TNFR_NGFR_1; 3.
PS50050; TNFR_NGFR_2; 3.
PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13:219-224(1992).
                                                                                                                                                                                                                                                                                                                     TRANSMEMBRANE;
              A38208
              JANES W., GENT, LESSLAUER W.;
                                                                                                                                                                                                                                                                                                                     GLYCOPROTEIN;
                                                                                                                                     CYTOPLASMIC (POTENTIAL).
4 X TNER-CYS.
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3.
                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR RECE
TUMOR NECROSIS FACTOR BIND
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                   REPEAT;
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                                                                                                                                                                                                                                                                                                                     SIGNAL;
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Best Local S
Matches 17
MEDLINE; 74011.
MEDLINE; 74011.
CARLSEN R.B., BAY
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21-JUL-1986 (REL. 01
01-OCT-1996 (REL. 34
CHORIOGONADOTROPIN E
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                                                                                                                                                                                  SEQUENCE OF MEDLINE; 8: BIRKEN S.,
                                                                                                                                                                                                                                                                   BOIME
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FIDDES J.C., GOODMAN H.M.
NATURE 286:684-687(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
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                                      PRELIMINARY SEQUENCE MEDLINE; 74011267.
                                                                                                                                                                                                                                                                                POLICASTRO P.,
                                                                                                                                                                                                                                                                                                                                                 NATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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NE; 84093590.
DGE K., VAMVAKOPOUL
E 307:37-40(1984).
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l Similarity 100.0%;
171; Conservative
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81117268.
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SEQUENCE OF 21-165.

MEDLLNE; 75211304.

MORGAN F.; BIRKEN S., CANFIELD R.E.;

J. BIOL. CHEM. 250:5247-5258(1975).
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                                                                                                                                                 ., FETHERSTON J., CANFIELD R.E., CHEM. 256:1816-1823(1981).
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BAHL O.P., SWAMINATHAN N.; 248:6810-6827(1973).
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01, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
34 CHAIN PRECURSOR (CHORIONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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                                           21-165
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GPAA -> APP (IN REF. 4
GPAACECRAOSE CRC32;
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Pred. No. 6.45e-296;
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R PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

R HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.

SIGNAL 1 20

CHAIN 21 165

CHORIOGONADOTROPII

DISULFID 29 77

DISULFID 43 92

DISULFID 46 130

DISULFID 46 130

DISULFID 46 130
                                                        Matches
                                                                   Query Match
Best Local :
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EMBL; J00117; G180437; -.
EMBL; M13504; G463088; -.
EMBL; M13505; G463089; -.
EMBL; M13503; G463090; -.
EMBL; K03189; G180453; -.
EMBL; K03189; G180453; -.
EMBL; K03188; G180453; JOINED.
EMBL; K03188; G180453; JOINED.
PIR; A01502; KTHUB.
PDB; 1HCN; 30-SEP-94.
PDB; 1HRP; 01-NOV-94.
                                                                                                      VARIANT
SEQUENCE
                                                                                                                                                                                                DISULFID DISULFID
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MISE T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W., CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.; NATURE 369:455-461(1994).

-I- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-5 FROM N.A.
MEDLINE; 86195987.
POLICASTRO P.F. DANIELS-MCQUEEN S.,
J. BIOL. CHEM. 261:5907-5916(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92314469.
WEISSHAAR G., HIY!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90094415.
SACCUZO BEEBE J., MOUNTJOY K., KRZESICKI R.F.,
                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    x-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCOBIOLOGY 1:393-404(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RUDDON R.W.;
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              198
                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUTROPIN, FOLLITROPIN AND GONADOTROPIN. TISSUE SPECIFICITY: PLACENTA.
             PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
                      PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
                                                       ch 40.5%;
1 Similarity 100.0%;
139; Conservative
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CHEM. 256:6587-6592(1981).
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17739
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                                                                                                       WW.
                                                      Score 1030; DB 1;
Pred. No. 1.12e-221;
0; Mismatches 0;
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FF1D4802
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                                                                              Length 165;
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P50555;
01-OCT-1996 (REL. 3
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01-NOV-1997 (REL. 3
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PROSITE; F
PROSITE; F
RECEPTOR;
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-!- SUBGUIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF TWFRI LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNERIC COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUTER B., PAULI U.H.;
GENE 163:263-266(1995)
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                                                                                                                                                                                                                                                                                                               TISSUE-KIDNEY;
MEDLINE; 96011645.
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                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                     TRANSMEMBRANE;
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34, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
CTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                       CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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 POTENTIAL.
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MEDLINE; 94
BEBO B.F.,
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MEDILINE; 91285014.
BARRETT K., TAYLOR-FISHWICK D.A., COEGRAY P.W., FELDMANN M., FOXWELL B.M., GUR, J. IMMUNOL, 21:1649-1656(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
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01-MAY-1992 (REL.
01-NOV-1997 (REL.
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                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 93156721.
                                                                                                                                                                                                                                                                                   MEDLINE: 94245292.
BEBO B.F., LINTHICUM D.S.;
IMMUNOGENETICS 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92039815.
ROTHE J.G., BROCKHAUS M.,
IMMUNOGENETICS 34:338-340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOODWIN R.G., ANDERSON D., JERZY R., DAV COPELAND N.G., JENKINS N.A., SMITH C.A., MOL. CELL. BIOL. 11:3020-3026(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., R
WONG G.H., CHEN E.Y., GOEDDEL D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WONG G.H., CHEN E. PROC. NATL. ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR
TNFR1 OR TNFR-1.
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                                                                                                                                                                                                         ROTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
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                HE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;

IMMUNOL. 30:165-175(1993).

FUNCTION: RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THER! LEAF HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPATSETRNDFQDTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQVRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KONTYCTCHAGFFLRENECYSCSNCKKSLECTKLCLPQIENYKGTEDSGTT 193
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125; Conser
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461 AA;
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llarity 73.1%;
Conservative
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50696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                                                                                                                                                                                                                                                                         GENTZ R., LESSLAUER W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1028; DB 1;
Pred. No. 3.59e-221;
24; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
8E2C350A CRC32;
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                     DEATH DOMAINS
                                        OF TNFR1 LEADS
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RESULT TUR1_RAT
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Best Local S
Matches 11
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EMBL; M59377; G202097; ...
EMBL; X59238; G5379; ...
EMBL; X57796; G54849; ...
EMBL; X57796; G4849; ...
EMBL; M6656; G202102; JOINI
EMBL; M68067; G202102; JOINI
EMBL; M76655; G202102; JOINI
EMBL; M76656; G202102; JOINI
EMBL; M76666; G202102; JOINI
EMBL; M76666; M7666; M7666; M766
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CONFLICT
SEQUENCE
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TRANSMEM
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PROSITE; PS00652; TNFR
PROSITE; PS50050; TNFR
PROSITE; PS50017; DEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR;
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR CONTAINS A LA-NGER/TNER-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                            DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
                                                                                                                                                                         DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             454
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      TNFR_NGFR_2; 3.
DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR_NGFR_1; 3.
                                                                                                                                                                                                                                                                                                                                                               37.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                                                                                                                                                                                                                        Score 960; DB 1; Le
Pred. No. 5.34e-204;
27; Mismatches 26;
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                PRT;
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                461
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CRC32;
              ₹
                                                                                                                                                                                                                                                                                                                                                                                  Length 454;
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                                              Query Match
Best Local Simi
Matches 115;
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01-AUG-1991 (REL. 1
01-MAR-1992 (REL. 2
01-NOV-1997 (REL. 2
TUMOR NECROSIS FACT
                                                                                                                                               REPEAT
REPEAT
REPEAT
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LANTE M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;

DNA CELL BIOL. 9.705-715(1990).

-I- FUNCTION: RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE FADD

RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING

AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE

SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE

PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

-I- SUBUNIT: THF BINDING TO THE EXTRACELLULAR DOMAIN OF THEN LEADS TO

HOMOTRIVERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-THERECRUITED TO

TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

NEL-ZABBA B CIANALTY OF TRADD SIGNALING CASCADES, APOPTOSIS AND
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                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
CHAIN
                                                                                                       CARBOHYD
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PIR; B36555; B36555.
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                                                                                                                           CARBOHYD
                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LANTZ
                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR;
  23
                      41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NF-KAPPA B SIGNALING (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
             DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P19438;
                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                PS00652; TNFR_NGFR_1; 3. PS50050; TNFR_NGFR_2; 3. PS50017; DEATH_DOMAIN; 1
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                                                                                          37.2%;
larity 67.3%;
Conservative
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21,
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A; CHORDATA;
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)

RECEPTOR 1 PRECURSOR (P
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                                              Score
Pred.
25; M
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4 X TNFR-CYS.
TNFR-CYS 1.
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DEATH DOMAIN
                                                                                                                                                                                                                                                                                                  TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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                                             re 944; DB 1; Le
d. No. 5.76e-200;
Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT; SIGNAL; APOPTOSIS
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                                                                                                                                                                                                                                                                                                                                                                               FACTOR RECEPTOR 1
                                                                  Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADOLF
                                              Indels
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Best Local S
Matches 11
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01-APR-1988 (REL. 07
01-OCT-1996 (REL. 34
CHORIOGONADOTROPIN E
                                                                                                                                                                                                                                                                                                              CARBOHYD
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CRAWFORD R.J., TREGEA
GENE 46:161-169(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPIO ANUBIS
EUKARYOTA; MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGHB_PAPAN P07434;
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M14966; G1765
PIR; A25808; KTBAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA;
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 318
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                                                                                                           87
                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROID ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THERE ARE AT LEAST FIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TWO OF THESE ARE EXPRESSED
                                                                                                                                            SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE
 SLPSPSRLPGPSDTPILPQ 336
                                    SPPSPSRLLEPAGTPFLPQ 165
                                                                           IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP
                                                                                        IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSSKDPPP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAZOA;
                                                                                                                                                                                                                                                                                              165
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1HCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G176573;
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                                                                                                                                                                                                                                                                                              ΑA,
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07, LAST SEQUENCE UPI
34, LAST ANNOTATION U
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PRECURSOR (CHORIONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERTEBRATA;
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                                                                                                                                                                                                                                                                                              78987D30
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                    857;
No. 4.
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1.26e-178;
tches 12;
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                                                                                                                                                                                                                                                      Length 165;
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                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                         -!- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM. EMBL; X00264; E28368; -. EMBL; S71273; E91454; -. EMBL; S71273; E91454; -. PIR; A01497; UTHUB. HSSP; P01233; 1HCN. MIM; 152780; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEISS J., ARELING TAMESON J.L.;

JAMESON J.L.;

PROMOTES SPERMATOGENES

TO SYNTH!
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MEDLINE; 84093590.
TALMADGE K., VAMVAKOPOULOS
NATURE 307:37-40(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOY-1995 (REL. 32, LAST ANNOTATION UPDATE)
LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92085985. WEISS J., AXELROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAIRAM M.R., LI C.H.;
BIOCHIM. BIOPHYS. ACTA 412:70-81(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSHB_HUMAN
P01229;
                                                                                                                                                                      SIGNAL
                                                                                                                                                                                          HORMONE; GLYCOPRODISEASE MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE OF CARBOHYDRATE. MEDLINE; 91122088.
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CLOSSET J., HENNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 21-141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEUTMANN H.T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATIN THE TESTES AND OVARIES TO SYMPHESIZE STEROIDS.
SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: PITUITARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHAAR G., HIYAMA J., RENWICK A.G.
J. BIOCHEM. 195:257-268(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDOCRINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARG-74
                                                                                                                                                                                                         PS00261; GLYCO_HORMONE_BETA_1; 1.
PS00689; GLYCO_HORMONE_BETA_2; 1.
GLYCOPROTEIN; SIGNAL; PSEUDOHERMAPHRODITISM;
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, PARLOW A.F.;
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METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29:97-100(1973).
  HUA Q.-X., WEISS M
L. 6:904-913(1992).
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                 LUTROPIN BETA CHAIN.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.A.;
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Best Local
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P51500;
01-OCT-1996
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CONFLICT
SEQUENCE
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CARBOHYD
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIDLINE; 96115012.

SIMULA A.P., AMATO F., FAAST R., LOPATA A., BERKA J., NORMAN R.J.;
BIOL. REPROD. 53:380-389(1995).

-I- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THE
ARE ESSENTIAL FOR THE MAINTENANCE OF PEGNANCY.

-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALLITHRIX JACCHUS EUKARYOTA; METAZOA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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                                                                                                                                                                                                                                                                         CARBOHYD
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    258
                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
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                     87
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                                                                                                                        27
                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: PLACENTA.
L; U04447; G606607; -.
                                                                                                     PLCRPVNAILAAEKEGCPVCVAFNTTICAGYCSSMVRVLQTILPPLPQSVCNYHELRFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDHPQL 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP
                                                                              PRCRPINATLAVEKEGCPYCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
                                                                                                                                                                 Similarity
90; Conser
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92; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOPROTEIN;
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141 AA;
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(REL.
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76
135
15345 .
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34, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
N BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
                                                                                                                                                                                                                                                                                         164
77
92
130
108
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146
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; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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17712
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64.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
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                                                                                                                                                                                                                                                 WW;
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                                                                                                                                                                                                                                                              BY SIMILARITY.
CHORIGONADOTROPIN B
BY SIMILARITY.
                                                                                                                                                            Score 709; DB 1; I
Pred. No. 3.56e-141;
25; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q -> R (IN HYPOGON

RECEPTOR-BINDING).

E -> Q (IN REF. 2)

MISSING (IN REF. 2

HPQL -> PQH (IN REF. 4)

HPQL -> PQH (IN REF. 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 740; DB 1; L
Pred. No. 7.12e-149;
                                                                                                                                                                                                                                                 E36A4DB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q (IN REF. 2
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PQH (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
                                                                                                                                                                                                                                                 CRC32;
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Best Local S
Matches 8
      LSHB_BOVIN
P04651;
13-AUG-1987
01-JAN-1988
01-OCT-1996
LUTROPIN BET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSHB_EQUAS
P19794;
01-FEB-1991
01-NOV-1995
01-OCT-1996
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CHAIN
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PROSITE;
HORMONE;
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J. MOL. ENDOCRINOL. 4:143-150(1990).

-I- FUNCTION: PROMOTES SPERMATGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROLDS.

-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, FOLLITROPIN AND GONADOTROPIN.

LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

EMBL; X80116; G510971; -.

EMBL; X53669; E27544; ALT_SEQ.

PIR: S15676; E27544; ALT_SEQ.
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SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUUS ASINUS (DONKEY).
EUKARYOTA; METAZOA; CH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-PLACENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUTROPIN/CHORIOGONADOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318
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                                                                                                                                                                                                                                              QPLTSTSTPTPGAS 157
                                                                                                                                                                                                                                                                                                             IRLPGCPPGVDPMVSFPVALSCHCGPCRLKTTDCGGPRDHPLACA-P--OTSSSCKDPPS
                                                                                                                                                                                                                                                                                                                                                                          SLPSPSRLPGPSDTPILPQ
                                                                                                                                                                                                        -SLPSPS-RLPGPS 329
                                                                                                                                                                                                                                                                                         IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E; PS00261; GLYCO_HORMONE_BETA_1; 1.
E; PS00689; GLYCO_HORMONE_BETA_2; 1.
E; GLYCOPROTEIN; SIGNAL.
E; GLYCOPROTEIN; SIGNAL.
1 20 BY SIMILARITY.
21 169 LUTROPIN/CHORIO.
21 169 LUTROPIN/CHORIO.
21 169 LUTROPIN/CHORIO.
21 169 SIMILARITY.
22 77 BY SIMILARITY.
23 12 BY SIMILARITY.
24 108 BY SIMILARITY.
25 110 BY SIMILARITY.
26 110 BY SIMILARITY.
27 12 12 BY SIMILARITY.
28 110 BY SIMILARITY.
29 110 BY SIMILARITY.
20 110 BY SIMILARITY.
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85; Conser
           BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; METAZOA; CHORDATA; PERISSODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REL. 17, CREATED)
(REL. 32, LAST SEQUENCE UI
(REL. 34, LAST ANNOTATION
(REL. 05, CREATED)
(REL. 06, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
FA CHAIN PRECURSOR (LUTEINIZING HORMONE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
54
58
113
33
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larity 63.4%;
Conservative
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                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 630; DB 1;
Pred. No. 1.18e-1;
21; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                  PRT;
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                                                                                                                  141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STEWART F.;
J DATA BANKS
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         (LSH-B) (LH-B).
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                               CARBOHYD
CONFLICT
CONFLICT
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                              DISULFID DISULFID DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
PROSITE;
HORMONE;
              EUKARYOTA;
EUTHERIA; [
[1]
                                                         ISHB_HORSE STANDARD; PRT; 169 AA. P08751; P01234; 01-AUG-1988 (REL. 08, CREATED) 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGHUIN-ROGISTER G., HENNEN G.;
EUR. J. BIOCHEM. 39:235-253(1973).

-I. FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

-I. SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLTROPIN AND GONADOTROPIN.

EMBL; M10077; G163301: -.

EMBL; M11506; G163299; -.
                   EQUUS CABALLUS (HORSE).
EUKARYOTA; METAZOA; CHORI
EUTHERIA; PERISSODACTYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHB.
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHO
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A01499; UTBOB. HSSP; P01233; 1HCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 21-139. MEDLINE; 74075724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 851
MAURER R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                      27
                                                                                                                                                            258
                                                                                                                                                                                                    198
                                                                                                                                                                     87 VRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137
                                                                                                                                                                                                             PLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELRFAS
                                                                                                                                                            IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD
                                                                                                                                                                                                   PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
                                                                                                                                                                                                                                             Similarity 72; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL;
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                                                                                                                                                                                                                                                                                       141 AA;
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M. 260:7072-7077(1985).
                                                                                                                                                                                                                                              Conservative
                              (HORSE).
AZOA; CHORDATA;
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                                                                                                                                                                                                                                                      24.28;
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                                                                                                                                                                                                                                                                                        MW.
                                                                                                                                                                                                                                                                                   MISSING (IN REF. 2).

Q -> E (IN REF. 3).

P -> S (IN REF. 2).

GP -> PG (IN REF. 3).

Q -> E (IN REF. 3).

W; 82879D1F CRC32;
                                                                                                                                                                                                                                                                                                                                                            LUTROPIN BETA C
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                            Score 614; DB 1; I
Pred. No. 1.01e-117;
22; Mismatches 17;
                               VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                            BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF. 2).
3.3).
2).
F. 3).
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                                                              (LSH-B/CG-B)
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Best Local
                                                                                                                                                         Matches
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SHERMAN G.B., WOLI
THREADGILL D.S., (
MOL. ENDOCRINOL.
LSHB_SHEEP
P01231;
21-JUL-1986
01-NOV-1995
                                                                                                                                                                                                                                  CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                         PROSITE;
PROSITE;
HORMONE;
SIGNAL
                                                                                                                                                                                                                  DISULFID DISULFID
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE OF CARBOHYDRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHORIOGONADOTROPIN, PARTIAL SEQUE WARD D.N., MOORE W.T. JR., BURLEI J. PROTEIN CHEM. 1:263-280(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUGINO H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 21-169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOUSFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 21-169.
MEDLINE; 87250476.
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                                                                                                                                                                 Local
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                                                                         OPLISTSTPTPGAS
                                                                                                                       PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
                                                                                                                                 PLCRPINATLAAEKEACPICITETTSICAGYCPSMVRVMPAALPAIPQPVCTYRELREAS 86
                                                                                                  -SLPSPS-RLPGPS
                                                                                        IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317
                                                                                                                                                          Similarity
84; Conser
                                                                                                                                                                                                                                                                                PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., BOUSFIELD G.R., MOORE W.T. CHEM. 262:8603-8609(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D G.R., LIU W.-K., SUGINO H., CHEM. 262:8610-8620(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87250475
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(REL.
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3
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3
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                                                                                                                                                                                         A
                         STANDARD;
01,
32,
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62.7%;
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77
92
130
108
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120
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CREATED)
LAST SEQUENCE UPDATE)
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                                                                                                                                                                                              LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
BY SIMILARITY.
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BURLEIGH B.D.;
                                                                                                                                                         Score
Pred.
22; M
                        PRT;
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                                                                                                                                                         Mismatches
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No. 1.
                        141
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                                                                                                                                                                 DB 1; Le
L.77e-117;
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                                                                                                                                                                        Length 169;
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5 B

27 198

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Query Match
Best Local
Matches
                                                   DISULFID
MOD_RES
CARBOHYD
VARIANT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                            CHAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
EMBL; $64695; G408241; -.
EMBL; X52488; G1320; -.
PIR; A01500; UTSHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 93351742.
BROWN P., MCNEILLY J.R., WALLACE R.M., MCNEILLY A.S.,
MOL. CELL. ENDOCRINOL. 93:157-165(1993).
                                                                                                                                                                                                                                               PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1. PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1. HORMONE; SIGNAL; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                           WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
EUR. J. BIOCHEM. 192:741-751(1990).

EUR. J. BIOCHEM. 192:741-751(1990).

TIPE TESTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 21-139.
MEDLINE; 73190035.
SAIRAM M.R., SAMY T.S.A.,
                                                                                                                                                                       DISULFID
                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                        PIR; A01500; UTSHB. PIR; S09232; S09232.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SAIRAM M.R., SAMY T.S.A., PAPKOFF H., LI C.H.; ARCH. BIOCHEM. BIOPHYS. 153:572-586(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 21-139.
MEDLINE; 72211145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 9024566
D'ANGELO-BERNARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHB.
OVIS ARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
                                                                                                                                                                                                                                                                              HSSP; P01233; 1HCN
                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE OF CARBOHYDRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. BIOL. CHEM. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PITUITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
h 23.7%;
Similarity 64.0%;
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHEEP).
METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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33
138
30
59
59
63
71
122
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54
54
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247:4365-4381(1972).
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                                                   141
59
63
72
123
123
                                           15184
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                                                  MISSING (IN SOME MOLECU)
Q -> E (IN REF. 1).
L -> P (IN REF. 2).
R -> Q (IN REF. 2).
PM -> PPM (IN REF. 4).
E -> Q (IN REF. 3 AND 4
Score 602; DB 1; L
Pred. No. 8.87e-115;
22; Mismatches 18;
                                                                                                                                                           LUTROPIN BETA CHAIN.
BY SIMILARITY.
                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BLOCKED.
                                           BA2C0204
                                          > PG (IN REF.
E (IN REF. 3
2C0204 CRC32;
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EF. 3 AND 4).
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                     Length 141;
 Indels
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Best Local S
Matches 7
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P01232;
21-UUL-1986 (REL. 01, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                             HORMONE;
SIGNAL
CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                            J. MOL.
[2]
                                                                                                                                             MOD_RES
                                                                                                                                                             DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 89306142.
KATO Y., HIRAI T.;
MOL. CELL. ENDOCRINOL.
                                                                                                                                                                                                                                                                    LUTROPIN, FOLLITROPIN AND GONADOTROPIN, EMBL; D00579; G217694; -. PIR; A30322; UTPGB. PIR; A48170; A48170.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 91063934. EZASHI T., HIRAI T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHB.
SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                               <del>-</del>
                                                                                                                                                                                                                                                                                                                                     MAGHUIN-ROGISTER G., HENNEN G.;
EUR. J. BIOCHEM. 39:235-253(1973)
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 21-139. MEDLINE; 74075724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA;
 258
                                198
                87
                                                27
                                                                                                                                                                                                                                                                                                    FUNCTION: PROMOTES SPERMATOGÈNESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYMPHESIZE STEDIDS.
SUBUNIT: HETERODIAGE OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRLPGCPPGVDPTVSFPVALSCHCGPCRLSSSDCGGPRAQPLACDRP 133
IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP
                                                                Similarity
71; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                    ENDOCRINOL.
                                                                                                                                                                                                                                           1233; 1HCN.
PS00261; GLYCO_HORMONE_BETA_1;
PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                     SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARTIODACTYLA.
                                                                                              141 AA;
                                                              23.5%;
larity 66.4%;
Conservative
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43
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77
92
130
108
110
120
33
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21
30
62
83
123
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                                                                                              14889
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                                                                                              MW;
                                                              Score
Pred.
19; M
                                                                                                                                                                   LUTROPIN BETA O
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                      BLOCKED.
R -> Z.
N -> D ()
V -> R ()
S -> I ()
I -> S ()
GP -> PG
                                                                 VERTEBRATA;
                                                               Mismatches
                                                                                                             S (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TETRAPODA;
                                                                                                                                                                                                                     CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            KATO
                                                                             Length 141;
                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308
                                                              0;
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                                                              Gaps
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RESULT
ID LA
AC P
DT 0
DT 0
DT 0

LSHB\_BALAC P33088; 01-OCT-1993 01-OCT-1993 01-OCT-1996

(REL. (REL.

27, CREATED)
27, LAST SEQUENCE UP
34, LAST ANNOTATION

UPDATE)

15

STANDARD;

PRT;

118

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                                                      В
                                                                       Query Match
Best Local S
Matches 7
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THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A U
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROT
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

EMBL; 7001542; 6758262; -.

R EMBL; 700749; G205176; -.

R EMBL; D00576; G220808; -.

R EMBL; D00576; G220808; -.

R PIR; 841527; 842527.

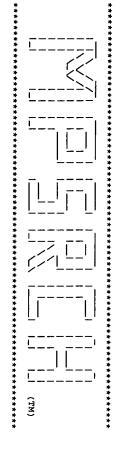
R HSSP; P01233; 1HCN.
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; Bout,
JAMESON L., CHIN
PTOL. CHEM. ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSHB_RAT
P01230;
21-JUL-1986
21-JUL-1986
01-OCT-1996
                                                                                                           DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLLNE: 85080043.
JAMESON L., CHIN W W., HOLLENBERG A.N
J. BIOL. CHEM. 259:15474-15480(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 83273673.
CHIN W.W., GODINE J.E.
                                                                                                                                                                                                                                                                                                                                                 STRAIN-WISTAR-IMAMICHI; TISSUE-ANTERIOR KATO Y., EZASHI T., HIRAI T., KATO T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHB
                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                               KATO Y., EZASHI
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 4-141
                                                                                                                                                                                                                                                                                                                                                                                                                                            HABENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUTROPIN
                                                                                                                                                                                                         HORMONE;
                                    198
 258
                  87
                                                      27
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          :|||||| ||:|:||:||:||:||:|| ||:::|||||::::|:||| |:::
IRLPGCPRGVNPVVSYAVALSCQCALCRRSTIDCGGPKDHPLICDDPRF
                                  Similarity
70; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                           J.F.;
                                                                                                                                                                                                         SIGNAL;
                                                                                                                                                                                                                PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RODENTIA.
                                                                                                                                                                                                                                                                                                                                        7:877-885(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GODINE J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REL. 01, CREATED)
(REL. 01, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
TA CHAIN PRECURSOR (LUTEINIZING HORMONE)
                                                                                                                             21
29
43
46
54
113
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                         GLYCOPROTEIN.
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141
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                                                                                23.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLEIN
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                                                                      Score 597;
Pred. No. 1.
23; Mismatc
                                                                                                                            LUTROPIN BETA CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                       PROBABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.R., CHANG A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                            6E0C19BA
                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
                                                                                 DB 1; L
..49e-113;
                                                                                                            CRC32
                                                                                                                                                                                                                                                                                                                                                         PITUITARY;
                                                                                                                                                                                                                                                                                                                                                                                              CHANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                             A.S.,
                                                                                                                                                                                                                                                                                                  IN AND A UNIQUE TO THYROTROPIN,
                                                                                          Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAN
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    L.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LSH-B) (LH-B).
                                                                                                                                                                                                                                                                                                                                                                                              HABENER
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                  135
 306
                                                                                                                                                                                                                                                                                                                              STIMULATING
                                                                       0
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                                                                      Gaps
                                    257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RR KARASEV V.S., PANKOY Y.A.;
RR KARASEV V.S., PANKOY Y.A.;
RL BIOKHMIIA 50:1972-1986(1985).
RC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC CHAIN WHICH COMPERS BIOCOCICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC PIR; P01233; 11CN.
CR PROSITE; P01233; 11CN.
CR PROSITE; P01233; 11CN.
CR PROSITE; P010261; GLYCO_HORMONE_BETA_2; FALSE_NEG.
CR PROSITE; P010261; GLYCO_HORMONE_BETA_2; FALSE_NEG.
CR PROSITE; P01039; GLYCO_HORMONE_BETA_1; 1.
CR PROSITE; P01030; GLYCO_HORMONE_BETA_2; FALSE_NEG.
CR PROSITE; P01030; GLYCO_HORMONE_BETA_1; 1.
CR PROSITE;
                                                                                                                                                                                                                                                                                                                                                       Query Match 23.4%;
Best Local Similarity 60.6%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LUTROPIN BETA CHAIN (LUTEINIZING HORMONE) (LSH-B). LHB.

BALABNOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

EUTHERIA; CETACEA.
                                                                                                                                                                                                                                          198
                                                                                                                      258
                                                                                                                                                                              67
                                                                                                                                                                                                                             6 09:03:50 1998
                                                                                                                                                                                                                                                                                                                                                       Score 595; DB 1; Le
Pred. No. 4.61e-113;
25; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 118;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                       ۲,
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                          1;
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Run on: MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Wed May 6 09:04:08 1998; MasPar time 17.16 Seconds 824.654 Million cell updates/sec

Tabular output not generated.

>US-08-804-166-8 (1-336) from US08804166.pep 2541 1 SRTSLLLAFGLLCLPWLQEG.....

Description: Perfect Score: Sequence: SRTSLLLAFGLLCLPWLQEG......PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150 Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 43.140; Variance 76.550; scale 0.564

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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20	18	17	16	15	14	13	12	11	10	မ	00	7	თ	. UI	4	ω	N	<u>, , .</u>	Result
289 271	294	301	303	304	306	312	321	353	361	391	430	582	595	596	945	975	1024	1024	Score
10.7	11.6	11.8	11.9	12.0	12.0		12.6		14.2	15.4	16.9	22.9	23.4	23.5	37.2	38.4	40.3	40.3	Query Match
101	147	150	138	138	138	130	130	137	147	80	140	141	139	135	180	471	165	145	Length
12 10	12	12	N	4	4	12	12	12	12	10	12	10	10	4	4	4	N	ν	BG
Q62590	013052	013051	Q16163	Q28376	P79357	Q98848	013050	Q90225	Q91121	Q63013	Q98849	260844	Q62778	019102	Q95185	019131	Q14000	013991	ID
THYROTROPIN BETA SUBUN BETA-THYROTROPIN (FRAG	THYROTROPIN BETA SUBUN	THYROTROPIN BETA SUBUN	THYROID-STIMULATING HO	THYROTROPIN BETA CHAIN	THYROTROPIN BETA CHAIN	GONADOTROPIN I BETA SU	GONADOTROPIN I BETA SU	GONADOTROPIN BETA-SUBU	GONADOTROPIN II BETA S	TESTICULAR LUTEINIZING	GONADOTROPIN II BETA S	LUTEINIZING HORMONE BE	TESTICULAR LUTEINIZING	LUTEINIZING HORMONE BE	TUMOUR NECROSIS FACTOR	TUMOR NECROSIS FACTOR-	CHORIONIC GONADOTROPIN	BETA-GONADOTROPIN.	Description
1.60e-37 9.17e-34	1.42e-38	4.73e-40	1.79e-40	1.10e-40	4.14e-41	2.21e-42	2.68e-44	3.56e-51	6.60e-53	1.91e-59	4.94e-68	3.51e-102	٠	2.28e-105	3.95e-186	3.72e-193	1.18e-204	1.18e-204	Pred. No.

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178	178	179	178	178	178	179	178	180	180	180	182	187	206	205	210	210	214	214	214	249	250	250	249	250	
7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.1	7.1	7.1	7.2	7.4	8.1	8.1	8.3	8. <sub>3</sub>	8.4	8.4		9.8					
440	440	425	411	411	411	401					259								348	426	418	380	277	253	
N	N	N	N	N	N	N	10	10	N	N	N	4	10	10	11	N	11	11	1	N	N	N	N	ν	
015531	014763	Q16042	014720	015508	015517	000300	Q63199	008727	014798	Q92956	014755	002764	Q62327	Q63012	085308	Q15962	089118	860680	Q85407	014865	000275	000280	014866	000276	
	APOPTOSIS INDUÇING REC	TUMOR NECROSIS FACTOR	DEATH RECEPTOR 5.	P53-REGULATED DNA DAMA	CYTOTOXIC TRAIL RECEPT	OSTEOPROTEGERIN.	FAS ANTIGEN PRECURSOR.	OSTEOPROTEGERIN.	CYTOTOXIC TRAIL RECEPT	HERPESVIRUS ENTRY MEDI	TRAIL RECEPTOR 3.	Ħ		TESTICULAR LUTEINIZING	SECRETED RECEPTOR BIND	THYROTROPIN BETA SUBUN		GARCIA-1966 RIGHT NEAR	HOMOLOG OF VACCINIA VI	DEATH RECEPTOR 3 BETA.	LYMPHOCYTE ASSOCIATED	LYMPHOCYTE ASSOCIATED	SOLUBLE DEATH RECEPTOR	LYMPHOCYTE ASSOCIATED	
3.24e-15	3.24e-15	2.10e-15	3.24e-15	3.24e-15	3.24e-15	2.10e-15	3.24e-15	1.36e-15	1.36e-15	1.36e-15	5.67e-16	6.32e-17	1.32e-20	2.07e-20	2.15e-21	2.15e-21	3.49e-22	3.49e-22	3.49e-22	3.14e-29	1.96e-29	1.96e-29	3.14e-29	1.96e-29	

# ALIGNMENTS

DT DT	Db Qy Db . Qy	Qu Be Ma Db	SO KW	AC CCC CCC CCC CCC CCC CCC CCC CCC CCC	RESULT
Q14000; Q14000; Q1-NOV-1996 Q1-NOV-1998 Q1-JAN-1998	67 258 127 318	Query Match Best Local Similarity Matches 138; Conse: 7 PRCRPINATLAVE	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 84093590. TALMADGE K., VAMVAKOPOU NATURE 307:37-40(1984). EMBL; X00266; E27486; - SIGNAL. SEQUENCE 145 AA; 154	991; NOV-199 NOV-199 NOV-199 NOV-199 A-GONAI O SAPII ARYOTA; HERIA;	ILT 1 Q13991
PRELIMINARY; PRT; 165 AA.  (TREMBLREL. 01, CREATED)  (TREMBLREL. 01, LAST SEQUENCE UPDATE (TREMBLREL. 05, LAST ANNOTATION UPDA	IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPPP	40.3%; Score 1024; 99.3%; Pred. No. 1.1 rvative 0; Mismatch KEGCPVCITVNTTICAGYCPTMT	LOS N.C., FIDDES 88 MW; AC321C60	L. 01, CREALL O1, LAST L. 01, LAST L. 01, LAST L. 01, LAST	PRELIMINARY; PRT; 145
); 165 AA.  ED) SEQUENCE UPDATE) ANNOTATION UPDATE)	PKDHPLTCDDPRFQASSSSKAPPP 126 	DB 2; Length 145; lBe-204; nes 1; Indels 0; Gaps 0; rRVLQGVLPALPQVVCNYRDVRFES 66	J.C.; GRC32;	TED) SEQUENCE UPDATE) ANNOTATION UPDATE) RTEBRATA; TETRAPODA; MAMMALIA;	AA.

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RESULT 4
ID Q95185
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ID 01
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Matches 13
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Best Local S
Matches 11
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019131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEE E.-K., TALYOR M.J., KEHRLI M.E.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL, U90937; GZ290398; -
PROSITE; PS00652; TNFR_NGFR_1; 3.
SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O1-JAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDAT
TUMOR NECROSIS FACTOR-RECEPTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           019131;
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EUTHERIA; I
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J. BIOL. CHEM. 258:11492-11499(1983).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHORIONIC
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POLICASTRO P., OVITT C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
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Local Similarity 99.3%;
es 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLPSPSRLPGPSDTPILPQ 165
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                                                                                                                                                                                RODTICHCHMGFFLKGAKCISCHDCKNK-ECEKLCPTRPSTGKDSQDPGTT:|:|:|| | | | ::|:||
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                                                                                                                                                                                                                                                                                                                                                                                                                           DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.4%; Score 975; DB 4; Length 471; larity 67.8%; Pred. No. 3.72e-193; Conservative 27; Mismatches 27; Indels
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          PRELIMINARY;
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Pred. No. 1.18e-204;
0; Mismatches 1;
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          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UPDATE)
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                                IRLPGCPPGVDPMVSFPVALSCRCGPCRLSSSDCGGPRAQPLACDRP
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Query Match
Best Local S
Matches 7
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Best Local S
Matches 11
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O1-JAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
LUTEINIZING HORMONE BETA SUBUNIT (FRAGMENT).
CURATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPED RHINOCEROS).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     095185;
01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQ
01-JAN-1998 (TREMBLREL. 05, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DUTHIE S., NASIR L., ECKERSALL P.D.; SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ EMBL; U72344; G1613880; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMOUR NECROSIS
TNFR-1.
                                                                                                                                                             SEQUENCE
                                                                                                                                                                           EMBL; U72659;
NON_TER
                                                                                                                                                                                          TISSUE-PITUITARY GLAND;
SHERMAN G.B., LUND L.A.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA
EMBL; U72659; G2462779; -.
                                                                                                                                                                                                                                                                                                                    SHERMAN G.B., LUND L.A., BUNICK D., GENE 195:131-139(1997).
                                                                                                                                                                                                                                                                                                                                                       TISSUE-PITUITARY GLAND;
MEDLINE; 97449288.
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Local Similarity 86.0%;
hes 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104
                  PLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPAAPQPVCTYHELRFAS 80
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PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
                                                                        23.5%;
Similarity 66.4%;
71; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 180
180 AA; 20399 MW; 5452A6B2 CRC32;
                                                                                                                                                           135 AA; 14212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                           MW;
                                                                          Score 596; DB 4; I
Pred. No. 2.28e-105;
20; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 945; DB 4; I
Pred. No. 3.95e-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                           F4F196D2 CRC32
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ANNOTATION UPDATE)
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Best Local :
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01-NOV-1996 (
01-JAN-1998 (
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01-NOV-1996
01-NOV-1996
01-NOV-1996
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Q60844
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Q62778
                                                                                                                                                                                       SUBMITTED (AUG-1995) TO EMBL; U25145; G930345; MGD; MGI:96782; LHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHANG F.P., RANNIKKO A., HUHTAN BIOCHEM. BIOPHYS. RES. COMMUN. EMBL; U25653; G915217; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-SPRAQUE DAWLEY;
MEDLINE; 95283549.
ZHANG F.P., RANNIKKO A
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-129 SVEV;
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EUKARYOTA; METAZOA; CHORDATA;
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
TESTICULAR LUTEINIZING I
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                        KAPUR V., MATZUK M.M.;
                                                                                                                                                                                                                                                                                EUKARYOTA;
                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                           260844;
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                                                                                                                                                                                                                                                                      EUTHERIA; RODENTIA.
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                                                                   87
                                                                                                 27 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELAFAS 86
                                                                                                                                             Local
                                           VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMACDLPHL 135
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IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 306
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                                                                                       PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
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                                                                                                                                   Similarity 68; Conser
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69; Conser
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) HORMONE BETA
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larity 62.4%;
Conservative
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   PRELIMINARY;
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                                                                                                                                                                                                                                                                               CHORDATA;
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                                                                                                                                                                                                                                                                                              01, CREATED)
01, LAST SEQUENCE UPDATE)
. 05, LAST ANNOTATION UPDATE)
. 07, THE NIZING HORMONE BETA-SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 01, CREATED)
. 01, LAST SEQUENCE UPDATE)
. 01, LAST ANNOTATION UPDATE)
HORMONE BETA-SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUHTANIEMI I.;
DMMUN. 210:858-865(1995).
                                                                                                                                Score 582; DB 10;
Pred. No. 3.51e-102;
24; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 595; DB 10;
Pred. No. 3.86e-105;
24; Mismatches 16;
   PRT;
                                                                                                                                                                                                                                                                               VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                             DATA BANKS
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ID Q91121
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                                                                                                                                                                           Query Match
Best Local Similarity
Matches 45; Conser
                                                                                                                                                                                                        MEDLINE; 9528339.

ZHANG F.P., RANNIKKO A., HUHTANALL BIOCHEM, BIOPHYS. RES. COMMUN. 21

EMBL; U25803; 6904026; -.

PENTENCE 80 AA; 8515 MW; 74F.
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Best Local S
 Q91121;
01-NOV-1996
01-NOV-1996
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01-NOV-1996 (
01-NOV-1996 (
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Q63013
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01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDAT
GONADOTROPIN II BETA SUBUNIT PRECURSOR.
CARASSIUS AURATUS (COLDETIS).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES;
                                                                                                                                                                                                                                                                                                                       RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (OCT-1996) TO EMBL; D88024; G1644243;
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OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES
                                                                                                                                                                                                                                                                 STRAIN-SPRAQUE DAWLEY;
MEDLINE; 95283549.
                                                                                                                                                                                                                                                                                                                                               TLHB3.
                                                                                                                                                                                                                                                                                                                                                        TESTICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOSHIURA Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-PITUITARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
                                                                                       292
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                                                                                                  60 GGPRTQPMTCDLPHL
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                                                                                                                                MTRVLQGVLFALFQVVCNYRDVRFESIRLFGCFRGVNFVVSYAVALSCQCALCRRSTTDC 291
                                                                                                                                             GGPKDHPLTCDDPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 16.9%;
Similarity 50.0%;
54; Conservative
                                                                                                                                                                                                                                                                                                              RODENTIA
                                                                                                                                                                                                                                                                                                                                                       96 (TREMBLREL.
96 (TREMBLREL.
96 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
24
140
 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KOBAYASHI M.,
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ;
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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140
15533 »
                                                                                                                                                                                     15.4%;
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                                                                                                            74
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. 01, LAST SEQUENCE UPDATE)
. 01, LAST ANNOTATION UPDATE)
HORMONE BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M., KATO Y., AIDA I
EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                        HUHTANIEMI I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Æ;
                                                                                                                                                                          Score 391; DB 10
Pred. No. 1.91e-1
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 430; DB 12;
Pred. No. 4.94e-68;
22; Mismatches 32;
CREATED)
LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                        74FA772D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GONADOTROPIN II E
7205FD03 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                          PRT;
                                                                                                                                                                                                                                                                                                                         VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                            210:858-865(1995).
                                           147
                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                     DB 10;
.91e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BETA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 140;
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RESULT
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Best Local S
Matches 4
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Best Local S
Matches 4
013050;
01-JUL-1997 (TREMBLREL. 04, CREA
01-JUL-1997 (TREMBLREL. 04, LAST
01-JUL-1997 (TREMBLREL. 04, LAST
GONADOTROPIN I BETA SUBUNIT PREC
CYPRINUS CARPIO (COMMON CARP).
EUKARYOTA; METAZOA; CHORDATA; VE
OSTEICHTHYES; ACTINOPTERYGII; CY
[1]
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SEQUENCE
                                                                                                                                                                                                                                                                          LT 12
013050
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TSAIH H.J., YANG L.T.;

SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; L11722; G437308; -.

SEQUENCE 137 AA; 15330 MW; F87577B5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL 01
01-NOV-1996 (TREMBLREL 01
01-NOV-1996 (TREMBLREL 01
GONADOTROPIN BETA-SUBUNIT.
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Q90225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACANTHOPAGRUS LATUS.
EUKARYOTA; ANIMALIA; METAZOA;
ACTINOPTERYGII; PERCIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q90225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. MOL. ENDOCH
EMBL; L35096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-PITUITARY GLAND;
MEDLINE; 96020549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORONE SAXATILIS (STRIPED BASS)
EUKARYOTA; METAZOA; CHORDATA; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) GONADOTROPIN II BETA SUBUNIT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HASSIN S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSTEICHTHYES;
                                                                                                                                                                                                                                                                                                                                                                                    258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198
                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 FELPDCPPGVDPTVTYPVAQSCHCGRCAMDTSDCTFESLQPNFCMNDIPF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 PPCQLINQTVSLEKEGCPKCHPVETTICSGHCITKDPVIKIPFSNVVQHVCTYRDLHYKT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC-DDPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRCRPINATIAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
                                                                                                                                                                                                                                                                                                                                                                                                                                   FELPDCPLGVDPTVTYPVAVSCNCGLCAMDTSDCTFESLQPNFCMNDIPF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPCQLINQTVSLEKEGCPKCHPVETTICSGHCITKDPVMKTRY-VYQHV-CTYRDLHYKT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC-DDPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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15096; G598255;
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33
147,
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DOCRINOL. 15:23-35(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.2%;
llarity 44.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                          PRELIMINARY;
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147
16398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222
                                                                                                                                  04, CREATED)
04, LAST SEQUENCE UI
04, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 353; DB 12;
Pred. No. 3.56e-51;
22; Mismatches 36
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 361; DB 12;
Pred. No. 6.60e-53;
24; Mismatches 36
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GONADOTROPIN II
; 292F2F62 CRC3:
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                              CYPRINIFORMES
                                                    VERTEBRATA; PISCES; GNATHOSTOMATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATA; PISCES; GNATHOSTOMATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F87577B5 CRC32;
                                                                                                                                                                                                                                                                          130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC32
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SPARIDAE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
RRR RRC OCCUPANT
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ID QS
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RESULT 14
ID P79357
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Best Local S
Matches 4
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Best Local
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                                                                                                           P79357;
01-MAY-1997 (TREMBLREL. (
01-MAY-1997 (TREMBLREL. (
01-MAY-1997 (TREMBLREL. (
THYROTROPIN BETA CHAIN.
KANIA S.A.,
SUBMITTED (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GONADOTROPIN I BETA SUBUNIT PR
CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98848;
01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 13
Q98848
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KOBAYASHI M., IWASAKI M., KONDO H., YOSHIURA Y., WAT.
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                          SEQUENCE FROM N.A.
                                                                                   LAMA GLAMA (LLAMA).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL.
                           TISSUE-PITUITARY;
                                                                        EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D88023; G1644241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YOSHIURA Y., KOBAYASHI M., SUBMITTED (OCT-1996) TO EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-PITUITARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTEICHTHYES;
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Similarity 41.3%;
43; Conservat
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Similarity 40.48;
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ACTINOPTERYGII; CYPRINIFORMES
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ODOM T.F.;
EMBL/GENBANK/DDBJ
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PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                      Score 312; DB 12; 1
Pred. No. 2.21e-42;
23; Mismatches 37;
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Pred. No. 2.68e-44;
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24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
GONADOTROPIN I BETA SUBUNIT; 3C222BFD CRC32;
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GONADOTROPIN I BE
; 3D37E6B1 CRC32;
                                                                                   VERTEBRATA;
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                                                                                   TETRAPODA; MAMMALIA;
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EMBL; U89294; G1872550; -. SEQUENCE 138 AA; 15571 MW; 332E4E82 CRC32;

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ID Q28376
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Best Local Similarity 47.9%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.0%; Score 304; DB 4; Le Best Local Similarity 47.9%; Pred. No. 1.10e-40; Matches 46; Conservative 17; Mismatches 27;
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01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
THYROTROPIN BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-PITUITARY;
TISSUE-PITUITARY;
KANIA S.A., OLCHOWY T.W., FRANK L.A.;
SUBMITTED (MAR-1.996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U51789; G1262916; -.
SEQUENCE 138 AA; 15663 MW; 2DA6B024 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUUS CABALLUS (HORSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PERISSODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 KTVEIPGCPHHVTPYFSYPVAVSCKCGKCDTDYSDC 115
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256 ESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291
                                                                                                                                                                                                                                                                                       256 ESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291
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01, LAST SEQUENCE UPDATE)
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Pred. No. 4.14e-41;
18; Mismatches 26;
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